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NParch_nn n.a. n.a. database search, using Smith-Waterman algorithm
Run on: Mon Nov 23 17:14:21 1998; MasPar time 2656.31 seconds
Tabular output not generated.
Title: >US-08-468-011A-1
Description: (1-2003) from US08468011A.1
N.A. Sequence: 2003 1 GTTCTGCTGGGAGGCAAGATTCTGCTGGGAGGCAAGT 2003
Comp: CAACAGAGAGCCGCTGGTTCTAAACAGAGACTTAAAGCT
Scoring table: TABLE metric
Gap 50
Nmatch STD : Base 0 Query 0
Searched: 52174 seqs, 102186385 bases x 2
Post-processing: Minimum Match 0x
Listing first 1000 summaries
Database: emb155 ba 2.0m_bkg 3.0m_buul 4.0m_buul 5.0m_buul 6.0m_buul
7.0m_buul 8.0m_buul 9.0m_buul 10.0m_buul 11.0m_buul
genbank107
Database: 12:gb-ba 13:gb-bkg 14:gb-in 15:gb-em 16:gb-ro 17:gb-pat
18:gb-pat 19:gb-pat 20:gb-pat 21:gb-pat 22:gb-ro 23:gb-pat
24:gb-pat 25:gb-pat 26:gb-pat 27:gb-pat 28:gb-pat 29:gb-pat
Statistics: Mean 9.643; Variance 2.747; scale 3.510
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

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and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
C	1	1438	71.8	2641	20	G560316	Human STS SMC-11599	5.90e+02
C	2	1438	71.8	2641	20	G560316	Human STS SMC-11599	5.90e+02
C	3	1229	11.4	1980	21	HSPTR005	Human parathyroid hormone	4.97e+285
C	4	111	5.5	548	21	HSPTR003	Human parathyroid hormone	1.81e+115
C	5	95	4.7	795	21	HSPTR002	Human parathyroid hormone	2.76e+91
C	6	69	3.4	641	21	HSPTR001	Human parathyroid hormone	3.98e+58
C	7	47	2.3	589	21	HSPTR004	Human parathyroid hormone	4.19e+38
C	8	44	2.2	1977	22	RNU55836	Rattus norvegicus para	1.82e+26
C	9	44	2.2	1977	22	RNU55836	Rattus norvegicus para	1.82e+26
C	10	23	1.1	1626	22	RNU14031	Xenopus laevis mRNA fo	1.38e+03
C	11	23	1.1	1626	22	RNU14031	Xenopus laevis mRNA fo	1.38e+03
C	12	20	1.0	1248	16	XY14035	Xenopus laevis mRNA fo	5.77e+01
C	13	20	1.0	1248	16	XY14035	Xenopus laevis mRNA fo	5.77e+01
C	14	20	1.0	9850	21	H512822	Human DNA sequence fro	5.77e+01
C	15	18	0.9	1784	24	G050590	Human STS SMC-11599	5.90e+02
C	16	18	0.9	1784	24	G050590	Human STS SMC-11599	5.90e+02
C	17	18	0.9	288	27	H1282115	Human immunodeficiency	2.23e+01
C	18	18	0.9	288	27	H1282115	Human immunodeficiency	2.23e+01
C	19	18	0.9	352	24	G382524	Human immunodeficiency	2.23e+01
C	20	18	0.9	352	24	G382524	Human immunodeficiency	2.23e+01
C	21	19	0.9	408	27	HV052617	HIV-1 isolate 8521-681	3.74e+00
C	22	19	0.9	740	19	AD58947	Allium sativum clone A	3.74e+00
C	23	19	0.9	770	19	DS3887	Nicotiana glauca mRNA f	3.74e+00
C	24	18	0.9	635	27	RNU55836	Rattus norvegicus para	1.82e+26
C	25	18	0.9	635	27	RNU55836	Rattus norvegicus para	1.82e+26
C	26	18	0.9	931	19	T08NTRAI	Nicotiana tabacum SRI	2.23e+01
C	27	18	0.9	1057	15	RABCN2	Oryctolagus cuniculus	2.23e+01
C	28	18	0.9	1178	19	GMD40666	Glycine max biotin car	2.23e+01
C	29	18	0.9	1381	21	H580038	H. sapiens mRNA for SMC	2.23e+01
C	30	18	0.9	1832	21	H580038	H. sapiens mRNA for SMC	2.23e+01
C	31	18	0.9	2158	22	AB003147	Mus musculus mRNA for	2.23e+01
C	32	19	0.9	2388	22	RATATIA	Rat angiotensin recept	3.74e+00
C	33	18	0.9	2835	21	H581693	Homo sapiens (subclone	2.23e+01
C	34	18	0.9	3347	19	R1282115	Rat (clone) Pp3c3 high	2.23e+01
C	35	18	0.9	3347	19	R1282115	Rat (clone) Pp3c3 high	2.23e+01
C	36	19	0.9	3472	22	S66402	vascular AT1a angioten	3.74e+00
C	37	18	0.9	3634	19	Y1281	Y. lipolytica gene for	2.23e+01
C	38	18	0.9	4565	21	H5095311	Human pseudotubercula	2.23e+01
C	39	18	0.9	4565	21	H5095311	Human pseudotubercula	2.23e+01
C	40	19	0.9	5813	14	DN02471	D. melanogaster trachea	3.74e+00
C	41	18	0.9	6101	19	SCYNL400	S. cerevisiae chromoso	2.23e+01
C	42	18	0.9	6203	21	AB002858	Homo sapiens KIAA0398	2.23e+01
C	43	18	0.9	6203	21	AB002858	Homo sapiens KIAA0398	2.23e+01
C	44	18	0.9	9005	13	L282876	L. esculentum Lc-ma10 g	3.74e+00

C	45	19	0.9	10328	19	AF035536	Spinacia oleracea cold	3.74e+00
C	46	18	0.9	12268	27	BD070263	Borrelia burgdorferi	2.23e+01
C	47	18	0.9	12268	27	BD070263	Borrelia burgdorferi	2.23e+01
C	48	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	49	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	50	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	51	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	52	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	53	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	54	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	55	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	56	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	57	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	58	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	59	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	60	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	61	19	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	62	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	63	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	64	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	65	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	66	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	67	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	68	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	69	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	70	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	71	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	72	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	73	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	74	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	75	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	76	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	77	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	78	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	79	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	80	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	81	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	82	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	83	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	84	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	85	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	86	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	87	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	88	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	89	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	90	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	91	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	92	18	0.9	13051	12	AC004700	Homo sapiens chromoso	3.74e+00
C	93	17	0.8	20	17	I14356	Sequence 2 from patent	1.21e+02
C	94	17	0.8	20	17	I14356	Sequence 2 from patent	1.21e+02
C	95	16	0.8	70	16	AF031705	Centrocercus urophasian	5.90e+02

C	96	16	0.8	76	16	AF051707	Phasianus colchicus mi	5.90e+02
C	97	16	0.8	78	16	AF051706	Centrocercus urophasian	5.90e+02
C	98	16	0.8	111	27	HV1009998	Human Immunodeficiency	5.90e+02
C	99	17	0.8	127	24	HSMV100117	Human chromosome X STS	1.21e+02
C	100	16	0.8	154	22	RATPAC128	Rattus norvegicus SMC	5.90e+02
C	101	16	0.8	183	20	HSMFD34	Human MFD34 dinucleoti	5.90e+02
C	102	16	0.8	181	24	G04933	Human STS M5930	5.90e+02
C	103	16	0.8	181	24	G029717	Gallus gallus mRNA for	5.90e+02
C	104	16	0.8	181	24	G029717	Gallus gallus mRNA for	5.90e+02
C	105	17	0.8	205	16	HV1077148	Gallus gallus mRNA for	5.90e+02
C	106	16	0.8	209	16	HV1077148	Gallus gallus mRNA for	5.90e+02
C	107	16	0.8	211	20	HSD29R	H. sapiens CpG island D	5.90e+02
C	108	16	0.8	215	15	PCU46781	Physceter latumodoni micro	5.90e+02
C	109	17	0.8	215	15	PCU46781	Physceter latumodoni micro	5.90e+02
C	110	17	0.8	235	27	HV1033780	Human Immunodeficiency	5.90e+02
C	111	16	0.8	236	27	HV103780	Human Immunodeficiency	5.90e+02
C	112	16	0.8	261	20	HDMV02CM	Human T-cell receptor	5.90e+02
C	113	16	0.8	295	12	HSD29R	Human T-cell receptor	5.90e+02
C	114	16	0.8	295	12	HSD29R	Human T-cell receptor	5.90e+02
C	115	16	0.8	303	16	H74033	proB-RNA polymerase be	5.90e+02
C	116	16	0.8	306	16	H78234	Gallus gallus clone vg	5.90e+02
C	117	16	0.8	321	16	G05014617	Gallus gallus clone vg	5.90e+02
C	118	17	0.8	327	20	G25051	Human STS SMC-11599	5.90e+02
C	119	17	0.8	342	21	HMO312M3	Human STS SMC-11599	5.90e+02
C	120	17	0.8	342	21	HMO312M3	Human STS SMC-11599	5.90e+02
C	121	16	0.8	362	14	G09107	Human STS SMC-11599	5.90e+02
C	122	16	0.8	362	14	G09107	Human STS SMC-11599	5.90e+02
C	123	16	0.8	362	14	G09107	Human STS SMC-11599	5.90e+02
C	124	16	0.8	373	17	H013094	Rice mRNA for GOS gene	5.90e+02
C	125	16	0.8	373	24	H013098	Sequence 3 from Patent	5.90e+02
C	126	16	0.8	373	24	H013098	H. sapiens DNA segment	5.90e+02
C	127	16	0.8	381	20	HSD207009	Human STS SMC-11599	5.90e+02
C	128	16	0.8	381	20	HSD207009	Human STS SMC-11599	5.90e+02
C	129	16	0.8	400	24	G13851	H. sapiens telomeric DN	5.90e+02
C	130	16	0.8	400	24	G13851	Human STS SMC-12369	5.90e+02
C	131	16	0.8	400	24	G13851	Human STS SMC-12369	5.90e+02
C	132	16	0.8	420	20	HSD29R	Human STS SMC-12369	5.90e+02
C	133	16	0.8	434	24	HDMV7405	Human mRNA for SMC	5.90e+02
C	134	17	0.8	468	16	AF019341	Human STS SMC-12369	5.90e+02
C	135	17	0.8	468	16	AF019341	Necturus maculosus trip	5.90e+02
C	136	16	0.8	504	26	HSD29R	Human telomeric DN	5.90e+02
C	137	16	0.8	522	14	TCSTP00B	Human STS SMC-12369	5.90e+02
C	138	16	0.8	532	16	FC10B	P. tetrazona trypsinolys	5.90e+02
C	139	17	0.8	533	19	FC10B	Porphyria I intermedia	1.21e+02
C	140	16	0.8	619	22	HSD29R	Human STS SMC-12369	5.90e+02
C	141	16	0.8	619	22	HSD29R	Human STS SMC-12369	5.90e+02
C	142	16	0.8	619	22	HSD29R	Battus norvegicus pool	5.90e+02
C	143	16	0.8	619	22	HSD29R	Human gene for Ig light	5.90e+02
C	144	16	0.8	619	22	HSD29R	Foot and mouth disease	5.90e+02
C	145	16	0.8	619	22	HSD29R	Human STS SMC-12369	5.90e+02
C	146	17	0.8	705	17	A01333	Synthetic oligonucle	1.21e+02

[illegible]

249	16	0.8	1722	16	XELPHGP	Xenopus laevis histone	5.90e+02
250	17	0.8	1746	22	RATPHIP	Rattus norvegicus poxa	1.21e+02
251	17	0.8	1762	22	MUSPTTHOS	Mus musculus parathyro	1.21e+02
252	17	0.8	1776	24	DROPTILLOP	Drosophila melanogaste	1.21e+02
253	17	0.8	1800	17	MGV948A	Measles virus major c	1.21e+02
254	17	0.8	1810	27	VACV948A	Vaccinia virus major c	1.21e+02
255	17	0.8	1815	14	DRO19722	Drosophila melanogaste	1.21e+02
256	16	0.8	1825	15	GAT4505CB	Gat mRNA for cytocho	5.90e+02
257	17	0.8	1825	15	COT74505CB	Cot mRNA for cytocho	5.90e+02
258	17	0.8	1862	17	SEV14119	Sequence 1 from paten	1.21e+02
259	17	0.8	1863	17	117765	Sequence 2 from paten	1.21e+02
260	17	0.8	1878	15	OPOTHR	Opesamus parathyroid	1.21e+02
261	16	0.8	1878	15	OPOTHR	Opesamus parathyroid	1.21e+02
262	16	0.8	1883	21	HSS5BDS	Human placenta meso-	5.90e+02
263	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
264	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
265	17	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
266	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
267	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
268	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
269	17	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
270	17	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
271	17	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
272	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
273	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
274	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
275	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
276	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
277	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
278	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
279	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
280	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
281	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
282	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
283	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
284	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
285	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
286	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
287	16	0.8	1833	17	ED1579	DNA encoding new human	5.90e+02
288	17	0.8	1880	12	RONGLUCBA	Rumicoccus albino	1.21e+02
289	17	0.8	1880	12	ED2552	Glycine soja chloropla	1.21e+02
290	17	0.8	1881	19	SOTPCG03A	Mus musculus (129/87) cc	5.90e+02
291	16	0.8	1881	19	AT01925	Sequence 59 from Paten	5.90e+02
292	16	0.8	1881	19	AT01925	Sequence 59 from Paten	5.90e+02
293	16	0.8	1881	19	AT01925	Sequence 59 from Paten	5.90e+02
294	17	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02
295	17	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02
296	17	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02
297	16	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02
298	16	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02
299	16	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02
300	16	0.8	1880	19	KLM614	K. lactis (2159/112) MG	1.21e+02

C 351	17	0.8	3192.19	OSG05236	O. sativa (rice) gnos1	1.1e+02
C 352	17	0.8	3192.19	OSG05236	Mouse myoglobin	1.1e+02
C 353	17	0.8	3296.21	HMDGCT5	Human gene for LRT/In	1.21e+02
C 354	17	0.8	3302.27	AG098259	Avian rotavirus RNA	5.90e+02
C 355	16	0.8	3302.27	AG098259	Avian rotavirus RNA	5.90e+02
C 356	17	0.8	3395.32	AF257025	Bos taurus intercellu	1.1e+02
C 357	16	0.8	3398.15	AF257025	Bos taurus intercellu	1.1e+02
C 358	17	0.8	3408.22	RATSPSR	Rat substance p recept	1.21e+02
C 359	17	0.8	3408.22	RATSPSR	Rat substance p recept	1.21e+02
C 360	16	0.8	3417.22	HUN81GA	Rhizobium meliloti	5.90e+02
C 361	16	0.8	3431.15	BTDPAAPL	Beta-tau mRNA for poly	5.90e+02
C 362	16	0.8	3451.20	HUMADBR1	Human beta-2-adrenargi	5.90e+02
C 363	16	0.8	3500.13	AF093982	Homo sapiens Jax2 kina	5.90e+02
C 364	16	0.8	3500.13	AF093982	Homo sapiens Jax2 kina	5.90e+02
C 365	16	0.8	3525.32	AF011414	Mus musculus putative	5.90e+02
C 366	17	0.8	3629.15	BOVIBFBP	Bovine Interphosrecep	1.21e+02
C 367	19	0.8	3651.22	AF057556	Mus musculus UNC-51-1	5.90e+02
C 368	16	0.8	3651.22	AF057556	Mus musculus UNC-51-1	5.90e+02
C 369	16	0.8	3682.11	AC002404	Homo sapiens putative	1.1e+02
C 370	16	0.8	3689.32	AF011425	Mus musculus putative	5.90e+02
C 371	16	0.8	3694.17	SO1240	DNA containing pho pro	5.90e+02
C 372	17	0.8	3762.19	AF052084	Y. cerevisiae PHO8 gene	5.90e+02
C 373	17	0.8	3762.19	AF052084	Y. cerevisiae PHO8 gene	5.90e+02
C 374	16	0.8	3806.32	NUM9941	Mesocricetus auratus p	5.90e+02
C 375	17	0.8	3822.22	RNCK1A	Rat mRNA for voltage d	1.21e+02
C 376	16	0.8	3829.19	SCDSHG13	Saccharomyces cerevisi	5.90e+02
C 377	16	0.8	3877.22	AF094932	Rattus norvegicus 9-K	5.90e+02
C 378	16	0.8	3877.22	AF094932	Rattus norvegicus 9-K	5.90e+02
C 379	16	0.8	3946.32	AF068628	Mus musculus DNA cyclo	5.90e+02
C 380	17	0.8	3957.17	Z00726	Genomic DNA encoding p	1.21e+02
C 381	16	0.8	4012.22	AF094930	Agrobacterium tumefaci	5.90e+02
C 382	16	0.8	4012.22	AF094930	Agrobacterium tumefaci	5.90e+02
C 383	16	0.8	4029.12	SCU12015	Streptomyces clavulige	5.90e+02
C 384	16	0.8	4124.21	AB014584	Homo sapiens mRNA for	5.90e+02
C 385	16	0.8	4130.22	MPOH0A1	M. musculus mRNA for ph	1.21e+02
C 386	16	0.8	4130.22	MPOH0A1	M. musculus DNA cyclo	5.90e+02
C 387	16	0.8	4165.31	AF005516	Mus musculus DNA cyclo	5.90e+02
C 388	16	0.8	4195.32	AF068626	Mus musculus DNA cyclo	5.90e+02
C 389	16	0.8	4205.17	AI20027	Macrophage migration i	5.90e+02
C 390	17	0.8	4215.20	SPFH0A1	R. sapiens PHMA 1 mRNA	1.21e+02
C 391	17	0.8	4317.22	AF094933	Rattus norvegicus 9-K	5.90e+02
C 392	17	0.8	4347.27	SI004984	Simian Immunodeficienc	1.21e+02
C 393	17	0.8	4350.27	SI004985	Simian Immunodeficienc	1.21e+02
C 394	17	0.8	4351.27	SI004982	Simian Immunodeficienc	1.21e+02
C 395	17	0.8	4351.27	SI004986	Simian Immunodeficienc	1.21e+02
C 396	17	0.8	4351.27	SI004986	Simian Immunodeficienc	1.21e+02
C 397	17	0.8	4353.27	SI004987	Simian Immunodeficienc	1.21e+02
C 398	17	0.8	4353.27	SI004990	Simian Immunodeficienc	1.21e+02
C 399	17	0.8	4353.27	SI004991	Simian Immunodeficienc	1.21e+02
C 400	17	0.8	4357.27	SI004991	Simian Immunodeficienc	1.21e+02
C 401	16	0.8	4370.99	AF592445	Sequence 28 from PATES	5.90e+02

C453	17	0.8	5397	30	CONVDPBB	<i>Gerrilla gorilla</i> ADP-1	1.2e+02
C454	16	0.8	5084	32	PATNCR	<i>Reinhardtia</i> sp.	5.0e+02
C455	16	0.8	5504	19	ZMADRLSA	Maize alcohol dehydrog	5.0e+02
C456	16	0.8	6159	19	ADH1-Cm	3 maize DNA for Adh1-Cm	5.0e+02
C457	16	0.8	5737	33	ZMADH1CN	3 maize alcohol dehydro	5.0e+02
C458	16	0.8	5737	33	ZMADH1CN	3 maize alcohol dehydro	5.0e+02
C459	16	0.8	6382	14	DMEF57	<i>Drosophila</i> mRNA for ec	5.0e+02
C460	16	0.8	6313	27	BACSPFOFA	<i>Bacillus subtilis</i> spo	5.0e+02
C461	16	0.8	6555	32	THGCG	Tobacco mild green mos	5.0e+02
C462	16	0.8	6555	32	THGCG	Tobacco mild green mos	5.0e+02
C463	16	0.8	6437	37	GRUNLAP	<i>Gutierrezia</i> virus-1 RNA	5.0e+02
C464	16	0.8	6633	32	AF043285	Mus musculus ribosomal	5.0e+02
C465	16	0.8	6830	12	SP952326	<i>Synechococcus</i> POC7942	5.0e+02
C466	16	0.8	6830	12	SP952326	<i>Synechococcus</i> POC7942	5.0e+02
C467	16	0.8	7070	14	CEU92519	Sequence from Percent	5.0e+02
C468	16	0.8	7070	14	CEU92519	Sequence from Percent	5.0e+02
C469	16	0.8	7099	37	W08115801	Soil-borne wheat mosaic	5.0e+02
C470	16	0.8	7266	21	MS15801	Homo sapiens mRNA for	5.0e+02
C471	16	0.8	7556	32	AF021678	Mus musculus gene enco	1.2e+02
C472	16	0.8	7556	32	AF021678	Mus musculus gene enco	1.2e+02
C473	16	0.8	7556	32	RNP450NA	R. norvegicus CPV17 gen	1.2e+02
C474	17	0.8	7556	32	RNP450NA	R. norvegicus CPV17 gen	1.2e+02
C475	16	0.8	7594	21	AF007216	Homo sapiens sodium bl	5.0e+02
C476	16	0.8	7824	37	HPU11794	H. sapiens mRNA for pho	1.2e+02
C477	16	0.8	7851	32	HPU11794	H. sapiens mRNA for pho	1.2e+02
C478	16	0.8	7817	37	FPN5153A	Human papillomavirus t	5.0e+02
C479	16	0.8	8077	32	FPN5153B	Human papillomavirus t	5.0e+02
C480	16	0.8	8077	32	FPN5153B	Human papillomavirus t	5.0e+02
C481	16	0.8	8122	37	WVAIL	Rattus norvegicus rice	5.0e+02
C482	16	0.8	8122	37	WVMOVG	Flavivirus langat NS1	5.0e+02
C483	17	0.8	8504	32	MG87C018	nonstructural polyprot	5.0e+02
C484	17	0.8	8504	32	MG87C018	nonstructural polyprot	5.0e+02
C485	17	0.8	9037	12	HPMAYL	Mus mus germline Igg-3 c	1.2e+02
C486	16	0.8	9223	21	HSMP043	Varola virus (Garcia)	5.0e+02
C487	17	0.8	9223	21	HSMP043	Varola virus (Garcia)	5.0e+02
C488	17	0.8	9356	37	HPICRA	Human periodic typtop	5.0e+02
C489	16	0.8	9438	37	SVGAGAB	<i>Pseudomonas putida</i> pla	1.2e+02
C490	17	0.8	9675	37	SVGAGAB	<i>Pseudomonas putida</i> pla	1.2e+02
C491	17	0.8	9675	37	SVGAGAB	<i>Pseudomonas putida</i> pla	1.2e+02
C492	17	0.8	9966	37	SVGMP9AB	Repetit. C virus RNA	5.0e+02
C493	17	0.8	9966	37	SVGMP9AB	Repetit. C virus RNA	5.0e+02
C494	16	0.8	10121	12	AE001028	Simian immunodeficien	1.2e+02
C495	16	0.8	10121	12	AE001028	Simian immunodeficien	1.2e+02
C496	17	0.8	10246	37	SV6P6E1	<i>Archaeoglobus fulgidus</i>	5.0e+02
C497	17	0.8	10246	37	SV6P6E1	<i>Archaeoglobus fulgidus</i>	5.0e+02
C498	17	0.8	10246	37	SV6P6E1	<i>Archaeoglobus fulgidus</i>	5.0e+02
C499	17	0.8	10246	37	SV6P6E1	<i>Archaeoglobus fulgidus</i>	5.0e+02
C500	17	0.8	10246	37	SV6P6E1	<i>Archaeoglobus fulgidus</i>	5.0e+02
C501	17	0.8	10246	37	SV6P6E1	<i>Archaeoglobus fulgidus</i>	5.0e+02
C502	16	0.8	10428	12	EC2A000438	Escherichia coli K-12	5.0e+02
C503	16	0.8	10589	12	PCU61801	<i>Porphyromonas gingi</i>	5.0e+02

C 402	16	0.8	4405	15	0.8	SCDPTA	C. cerevisiae, HBDP1 gene	5.90e-02
C 403	16	0.8	4406	15	0.8	SCDPTA	Rabbit phosphatase 1	5.90e-02
C 404	16	0.8	4407	15	0.8	SCDPTA	Rabbit phosphatase 1	5.90e-02
C 405	17	0.8	4457	22	0.8	MAP2C9	M.musculus mRNA for ad	5.90e-02
C 406	17	0.8	4458	15	0.8	MAP2C9	Cryptosporidium cucullu	5.90e-02
C 407	16	0.8	4459	22	0.8	MAP2C9	Cryptosporidium cucullu	5.90e-02
C 408	17	0.8	4460	22	0.8	MAP2C9	Sequence 1 from patent	5.90e-02
C 409	16	0.8	4461	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 410	17	0.8	4462	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 411	17	0.8	4463	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 412	17	0.8	4464	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 413	17	0.8	4465	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 414	17	0.8	4466	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 415	17	0.8	4467	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 416	17	0.8	4468	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 417	17	0.8	4469	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 418	16	0.8	4470	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 419	16	0.8	4471	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 420	16	0.8	4472	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 421	16	0.8	4473	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 422	16	0.8	4474	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 423	16	0.8	4475	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 424	16	0.8	4476	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 425	16	0.8	4477	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 426	17	0.8	4478	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 427	17	0.8	4479	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 428	17	0.8	4480	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 429	17	0.8	4481	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 430	16	0.8	4482	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 431	16	0.8	4483	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 432	17	0.8	4484	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 433	17	0.8	4485	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 434	16	0.8	4486	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 435	16	0.8	4487	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 436	16	0.8	4488	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 437	16	0.8	4489	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 438	16	0.8	4490	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 439	16	0.8	4491	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 440	16	0.8	4492	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 441	16	0.8	4493	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 442	16	0.8	4494	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 443	16	0.8	4495	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 444	16	0.8	4496	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 445	17	0.8	4497	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 446	16	0.8	4498	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 447	16	0.8	4499	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 448	16	0.8	4500	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 449	17	0.8	4501	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 450	16	0.8	4502	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 451	16	0.8	4503	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 452	16	0.8	4504	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 453	16	0.8	4505	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 454	16	0.8	4506	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 455	16	0.8	4507	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 456	16	0.8	4508	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 457	16	0.8	4509	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 458	16	0.8	4510	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 459	16	0.8	4511	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 460	16	0.8	4512	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 461	16	0.8	4513	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 462	16	0.8	4514	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 463	16	0.8	4515	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 464	16	0.8	4516	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 465	16	0.8	4517	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 466	16	0.8	4518	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 467	16	0.8	4519	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 468	16	0.8	4520	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 469	16	0.8	4521	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 470	16	0.8	4522	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 471	16	0.8	4523	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 472	16	0.8	4524	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 473	16	0.8	4525	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 474	16	0.8	4526	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 475	16	0.8	4527	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 476	16	0.8	4528	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 477	16	0.8	4529	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 478	16	0.8	4530	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 479	16	0.8	4531	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 480	16	0.8	4532	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 481	16	0.8	4533	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 482	16	0.8	4534	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 483	16	0.8	4535	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 484	16	0.8	4536	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 485	16	0.8	4537	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 486	16	0.8	4538	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 487	16	0.8	4539	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 488	16	0.8	4540	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 489	16	0.8	4541	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 490	16	0.8	4542	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 491	16	0.8	4543	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 492	16	0.8	4544	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 493	16	0.8	4545	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 494	16	0.8	4546	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 495	16	0.8	4547	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 496	16	0.8	4548	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 497	16	0.8	4549	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 498	16	0.8	4550	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 499	16	0.8	4551	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 500	16	0.8	4552	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 501	16	0.8	4553	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 502	16	0.8	4554	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 503	16	0.8	4555	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 504	16	0.8	4556	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 505	16	0.8	4557	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 506	16	0.8	4558	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 507	16	0.8	4559	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 508	16	0.8	4560	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 509	16	0.8	4561	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 510	16	0.8	4562	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 511	16	0.8	4563	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 512	16	0.8	4564	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 513	16	0.8	4565	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 514	16	0.8	4566	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 515	16	0.8	4567	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 516	16	0.8	4568	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 517	16	0.8	4569	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 518	16	0.8	4570	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 519	16	0.8	4571	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 520	16	0.8	4572	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 521	16	0.8	4573	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 522	16	0.8	4574	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 523	16	0.8	4575	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 524	16	0.8	4576	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 525	16	0.8	4577	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 526	16	0.8	4578	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 527	16	0.8	4579	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 528	16	0.8	4580	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 529	16	0.8	4581	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 530	16	0.8	4582	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 531	16	0.8	4583	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 532	17	0.8	4584	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 533	17	0.8	4585	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 534	17	0.8	4586	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 535	16	0.8	4587	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 536	16	0.8	4588	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 537	16	0.8	4589	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 538	16	0.8	4590	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 539	16	0.8	4591	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 540	16	0.8	4592	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 541	16	0.8	4593	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 542	16	0.8	4594	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 543	16	0.8	4595	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 544	16	0.8	4596	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 545	16	0.8	4597	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 546	16	0.8	4598	22	0.8	MUSHROR2	Mus mus mus mus mus mus	5.90e-02
C 547	16	0.8	4599	22	0.8	M		

504	16	0.8	10620	16	AF052602	Danio rerio huntingtin
505	16	0.8	10921	16	AF050058	Human hsc70 corecpon
506	16	0.8	110921	16	HSPX005915	Helicobacter pylori ae
507	16	0.8	11069	11	HSPX005918	H.sapiens Pag gene
508	17	0.8	11162	12	CEK1A	Vibrio cholerae DNA fo
509	16	0.8	11162	12	CEK1A	Vibrio cholerae DNA fo
510	16	0.8	11246	12	AF001343	Citrobacterium kilaru ntp
511	17	0.8	11793	15	BOVIRBP	Bovine interpherocep
512	17	0.8	11802	15	HPA000030	Mycoplasma pneumoniae
513	16	0.8	11923	14	CEZF10C5	Cenorhabditis elegans
514	16	0.8	12015	12	CEZF10C5	Cenorhabditis elegans
515	16	0.8	12015	12	CEZF10C5	Cenorhabditis elegans
516	16	0.8	12447	16	AF021430	Fugu rubripes APP prot
517	16	0.8	12971	12	AE001700	Archaeoglobus fulgidus
518	16	0.8	13068	12	AE001700	Archaeoglobus fulgidus
519	16	0.8	13119	14	MG041832	Neurospora burgdorferi
520	16	0.8	13125	14	MG041832	Drosophila melanogaste
521	17	0.8	13968	12	AE009091	Methanobacterium therm
522	16	0.8	14052	12	HSC110158	H.sapiens DNA for cone
523	16	0.8	14052	12	HSC110158	H.sapiens DNA for cone
524	16	0.8	14561	12	U67549	Methanococcus jannasch
525	16	0.8	14925	12	MG041832	Mus musculus putative
526	19	0.8	15229	20	HM010034	Human JF germline H-ch
527	19	0.8	15229	20	HM010034	Human JF germline H-ch
528	16	0.8	15626	11	HS140101	Human DNA sequence for
529	16	0.8	15737	12	AF000709	Aquifex aeolicus secti
530	17	0.8	15913	11	HSALAD06	H.sapiens ALAD gene fo
531	17	0.8	16014	11	HSALAD06	H.sapiens ALAD gene fo
532	17	0.8	17704	20	HM040470	Neisseria meningitidis
533	17	0.8	17866	21	D49493	Neisseria meningitidis
534	16	0.8	18743	14	CEK1L1D5	Cenorhabditis elegans
535	16	0.8	18743	14	CEK1L1D5	Cenorhabditis elegans
536	16	0.8	18743	14	CEK1L1D5	Cenorhabditis elegans
537	16	0.8	20576	12	HPA000631	Helicobacter pylori ae
538	16	0.8	22214	21	CEK03455	Homo sapiens aldose re
539	16	0.8	22966	18	AF057013	Streptococcus thermoph
540	17	0.8	23500	20	HSCB1000	Human gene for cardiac
541	17	0.8	25000	20	HSCB1000	Human gene for cardiac
542	16	0.8	25869	21	AC002459	Human BAC clone R1880
543	16	0.8	32513	19	SC9510	S.cerevisiae chromosom
544	16	0.8	32513	19	SC9510	S.cerevisiae chromosom
545	16	0.8	36681	20	HSV14811	Human DNA sequence for
546	17	0.8	37102	14	CEZF15H12	Cenorhabditis elegans
547	16	0.8	37277	14	CEK05043	Cenorhabditis elegans
548	16	0.8	37770	14	CEK05043	Cenorhabditis elegans
549	16	0.8	37770	14	CEK05043	Cenorhabditis elegans
550	16	0.8	37858	21	HS11806B	Human DNA sequence for
551	17	0.8	27874	22	HM071085	Mus musculus insulin-1
552	16	0.8	28418	20	HM087177	Romo sapiens (clones 1
553	16	0.8	29103	14	CEZF5764	Cenorhabditis elegans
554	16	0.8	29103	14	CEZF5764	Cenorhabditis elegans

555	16	0.8	29363.14	SC57D6	<i>Cenorchabditis elegans</i>	5.90e+02
556	17	0.8	29366.19	SC57Y1X	<i>S. cerevisiae</i> chromosome	1.21e+02
557	16	0.8	29626.14	CELR153	<i>Cenorchabditis elegans</i>	5.90e+02
558	16	0.8	29672.33	SPACD14	<i>S. pombe</i> chromosome 1 c	5.90e+02
559	16	0.8	30034.99	CEU70841	<i>Caenorhabditis elegans</i>	5.90e+02
561	17	0.8	30288.37	CAU55001	<i>Oryza sativa putative</i>	1.21e+02
562	17	0.8	30288.37	CAU55001	<i>Canine adenovirus type</i>	1.21e+02
563	16	0.8	30500.14	CEM10212	<i>Cenorchabditis elegans</i>	5.90e+02
564	16	0.8	30500.14	CEM10212	<i>Neomorphabditis elegans</i>	5.90e+02
565	16	0.8	31102.31	AP031460	<i>Neomorphabditis elegans</i>	5.90e+02
566	16	0.8	31102.31	AP031460	<i>Neomorphabditis elegans</i>	5.90e+02
567	16	0.8	31250.20	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
568	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
569	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
570	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
571	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
572	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
573	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
574	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
575	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
576	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
577	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
578	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
579	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
580	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
581	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
582	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
583	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
584	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
585	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
586	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
587	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
588	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
589	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
590	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
591	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
592	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
593	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
594	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
595	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
596	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
597	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
598	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
599	16	0.8	31273.14	CEM05810	<i>Cenorchabditis elegans</i>	5.90e+02
600	17	0.8	38052.21	HSAC000163	<i>Human DNA sequence</i>	1.21e+02
601	16	0.8	38060.14	CEU13732	<i>Cenorchabditis elegans</i>	5.90e+02
602	17	0.8	38092.14	CEU13732	<i>Cenorchabditis elegans</i>	5.90e+02
603	17	0.8	38092.14	CEU13732	<i>Cenorchabditis elegans</i>	5.90e+02
604	17	0.8	38092.14	CEU13732	<i>Cenorchabditis elegans</i>	5.90e+02
605	17	0.8	38092.14	CEU13732	<i>Cenorchabditis elegans</i>	5.90e+02

C 605	16	0.8	39849	31	AC025346	Human sapiegna chromosome	5,906+02
C 606	16	0.8	39255	31	AC020496	Human Csmid g19x0A0074	5,906+02
C 608	16	0.8	39433	14	CEB0564	Cenorhabditis elegans	5,906+02
C 609	16	0.8	39412	21	HS02212	Human chromosome 10 cl	5,906+02
C 610	16	0.8	39413	21	HS02212	Human chromosome 10 cl	5,906+02
C 611	17	0.8	39511	30	CEB0463	Human Pirelli receptor	5,906+02
C 612	16	0.8	39512	31	DB6993	Human (lambda) DNA for	5,906+02
C 613	16	0.8	39805	14	CELR430	Cenorhabditis elegans	5,906+02
C 614	17	0.8	40057	31	AC041889	Human sapiegna clone UMG	5,906+02
C 615	16	0.8	40058	31	AC041889	Human sapiegna clone UMG	5,906+02
C 616	17	0.8	40433	31	HS022374	Human sapiegna clone UMG	5,906+02
C 617	16	0.8	40571	12	HS022376	Myco bacterium leprae c	5,906+02
C 618	16	0.8	40649	31	AC03111	Human DNA from chromos	5,906+02
C 619	16	0.8	40649	31	AC03111	Human DNA from chromos	5,906+02
C 620	17	0.8	40678	13	CEB1785	Cenorhabditis elegans	5,906+02
C 621	16	0.8	40889	14	CELM02B8	Cenorhabditis elegans	5,906+02
C 622	17	0.8	40896	24	CELM02B8	Cenorhabditis elegans	5,906+02
C 623	16	0.8	40910	21	CELM02B8	Cenorhabditis elegans	5,906+02
C 624	16	0.8	40910	21	CELM02B8	Cenorhabditis elegans	5,906+02
C 625	17	0.8	41322	14	CEB5086	Cenorhabditis elegans	5,906+02
C 626	16	0.8	41369	21	CELM15314	Human sapiegna DNA from	5,906+02
C 627	16	0.8	42031	14	CEB15345	Cenorhabditis elegans	5,906+02
C 628	16	0.8	42031	14	CEB15345	Cenorhabditis elegans	5,906+02
C 629	16	0.8	42633	14	CEB23912	Cenorhabditis elegans	5,906+02
C 630	17	0.8	42666	14	CEB23912	Cenorhabditis elegans	5,906+02
C 631	16	0.8	43051	21	AB001517	Human sapiegna DNA for T	5,906+02
C 632	16	0.8	43051	21	AB001517	Human sapiegna DNA for T	5,906+02
C 633	16	0.8	43568	31	AC005337	Human sapiegna chromosom	5,906+02
C 634	17	0.8	43731	21	AC005337	Genomic sequence from	5,906+02
C 635	16	0.8	43952	21	HS010564	Human DNA sequence fro	5,906+02
C 636	16	0.8	43952	21	HS010564	Human DNA sequence fro	5,906+02
C 637	17	0.8	44233	14	CEB25063	Cenorhabditis elegans	5,906+02
C 638	16	0.8	44233	14	CEB25063	Cenorhabditis elegans	5,906+02
C 639	16	0.8	44824	14	AC024774	Drosophila melanogaste	5,906+02
C 640	16	0.8	45110	13	AC005032	Human sapiegna clone LIL	5,906+02
C 641	16	0.8	45110	13	AC005032	Human sapiegna clone LIL	5,906+02
C 642	16	0.8	45505	21	CEB14237	Human sapiegna chromosom	5,906+02
C 643	16	0.8	46105	14	CEB25535	Cenorhabditis elegans	5,906+02
C 644	17	0.8	46275	21	AC002389	Human DNA from chromos	5,906+02
C 645	17	0.8	46275	21	AC002389	Human DNA from chromos	5,906+02
C 646	17	0.8	47520	20	HS025508	Human DNA sequence fro	5,906+02
C 647	16	0.8	47440	31	CEB13509	Human sapiegna csmid cl	5,906+02
C 648	16	0.8	47554	14	CEB12007	Cenorhabditis elegans	5,906+02
C 649	17	0.8	49268	21	AC023928	Human DNA from chromos	5,906+02
C 650	16	0.8	49268	21	AC023928	Human DNA from chromos	5,906+02
C 651	16	0.8	52384	31	CEB1982518	Human sapiegna DNA for	5,906+02
C 652	16	0.8	52397	18	CEB25518	Myco bacteriophage L5 c	5,906+02
C 653	16	0.8	56220	14	CEB25281	Cenorhabditis elegans	5,906+02
C 654	16	0.8	56260	21	CEB25281	Human sapiegna gene for	5,906+02
C 655	16	0.8	56260	21	CEB25281	Human sapiegna gene for	5,906+02

C	657	17	0.8	5988	2	AC004376	***. SQUORCYNUS H PROG
C	658	16	0.8	61989	93	YSC0R378	Saccharomyces cerevisiae
C	659	17	0.8	64215	21	AC000054	Human septins chromosome
C	660	17	0.8	65589	21	AC049895	Human septins nribin (1.12e+02)
C	661	16	0.8	65591	19	AC049895	Human septins nribin (1.12e+02)
C	662	16	0.8	69023	19	SCD8035	Saccharomyces cerevisiae
C	663	16	0.8	69060	21	AC005196	Human septins chromosome
C	664	16	0.8	69822	14	AC003121	Drosophila melanogaster
C	665	16	0.8	70028	19	AC005196	Human septins chromosome
C	666	16	0.8	70028	19	BP000030	Epistasis virgulinan on
C	667	16	0.8	73087	21	HS17419	Human septins DNA seqe
C	668	16	0.8	73118	13	CHS198223	Cenohorbattis elegans
C	669	16	0.8	73118	13	CHS198223	Human septins Xp21.1 (1.12e+02)
C	670	17	0.8	76146	31	BP26985	Human septins chromosome
C	671	16	0.8	76146	31	BP26985	Human septins chromosome
C	672	16	0.8	76146	31	AC005370	Human septins chromosome
C	673	16	0.8	76221	21	AC003109	Human DNA from overlap
C	674	16	0.8	76221	21	AC003109	Human DNA from overlap
C	675	17	0.8	79860	14	AC004249	Drosophila melanogaster
C	676	17	0.8	79876	19	AB008264	Arabidopsis thaliana
C	677	16	0.8	80343	21	HS574112	Human DNA sequence fro
C	678	16	0.8	80343	21	HS574112	Human DNA sequence fro
C	679	16	0.8	82001	19	AB005422	Arabidopsis thaliana
C	680	16	0.8	82551	21	AC004506	Human septins PAC clone
C	681	16	0.8	83079	21	AC004538	Human septins chromosome
C	682	16	0.8	84052	21	AC003006	Drosophila melanogaster
C	683	16	0.8	84052	21	AC003006	Drosophila melanogaster
C	684	16	0.8	84114	21	AC003006	Human DNA from overlap
C	685	16	0.8	84235	19	AB015475	Arabidopsis thaliana
C	686	16	0.8	84440	19	AB010075	Arabidopsis thaliana
C	687	16	0.8	85213	14	AC004331	Drosophila melanogaster
C	688	17	0.8	85213	14	AC004331	Drosophila melanogaster
C	689	16	0.8	85260	14	AC001661	Drosophila melanogaster
C	690	17	0.8	85590	21	HS453D15	Human septins DNA seqe
C	691	16	0.8	85590	21	HS453D15	Human septins DNA seqe
C	692	16	0.8	85590	21	AC004464	Human septins 19q13.1 p
C	693	16	0.8	86558	21	AC004464	Human DNA sequence fro
C	694	16	0.8	87013	21	HS52818	Human septins chromosome
C	695	17	0.8	87246	21	AC002539	Human septins chromosome
C	696	17	0.8	87246	21	AC002539	Human septins chromosome
C	697	16	0.8	88972	12	MUS38105	Mus musculus BTK locus
C	698	16	0.8	90731	21	AC004899	Human septins clone D30
C	699	16	0.8	90731	21	HS39993	Human septins DNA seqe
C	700	17	0.8	92663	16	AB010470	Drosophila melanogaster
C	701	17	0.8	92663	16	AB010470	Drosophila melanogaster
C	702	17	0.8	92663	16	GBE04025	Gallus gallus (Chicken
C	703	17	0.8	92948	19	ATAF006557	Arabidopsis thaliana B
C	704	16	0.8	93250	21	HS447B16	Human DNA sequence fro
C	705	16	0.8	93632	19	AC005248	Human septins X-linked
C	706	16	0.8	93632	19	AC005248	Human septins X-linked
C	707	17	0.8	94365	19	BAC F181A1 from Chino	Human septins X-linked

708	17	0.8	84365	31	HR645M16	Human DNA sequence ***	1.1e+02
709	16	0.8	84665	31	WGA0479	Human apolipoprotein D	5.9e+02
710	16	0.8	86273	33	CEH21C11	Ctenophorabittia elegans	5.9e+02
711	17	0.8	86589	33	HTF70N7	Arabidopsis thaliana D	1.2e+02
712	16	0.8	86721	31	HTF70N7	Human chromosome 19p13	5.9e+02
713	16	0.8	86721	31	HTF74R12	Human chromosome 19p13	5.9e+02
714	16	0.8	86543	31	AC005152	Human sapiens chromosome	5.9e+02
715	17	0.8	88454	34	AC005267	Drosophila melanogaster	1.2e+02
716	17	0.8	88454	34	AC005267	Human DNA from chromosome	1.2e+02
717	16	0.8	89613	31	AC024271	Human sapiens chromosome	5.9e+02
718	17	0.8	89848	33	AC004874	Human sapiens genomic D	1.2e+02
719	17	0.8	100000	31	AP000049	Human sapiens genomic D	1.2e+02
720	16	0.8	100000	31	AP000018	Human sapiens genomic D	1.2e+02
721	16	0.8	100000	31	AP000018	Human sapiens genomic D	1.2e+02
722	17	0.8	100314	19	PAMTPAC4	Podopsora anserina	5.9e+02
723	17	0.8	100314	19	PMTPAC3	Podopsora anserina	5.9e+02
724	16	0.8	100399	12	SS100BPR	S. enteritidis complete ml	1.2e+02
725	16	0.8	100399	12	SS100BPR	S. enteritidis complete ml	1.2e+02
726	16	0.8	100988	33	AC005072	Human sapiens chromosome	5.9e+02
727	16	0.8	101486	33	AC005228	Human sapiens chromosome	5.9e+02
728	16	0.8	101647	33	ATAC004665	Arabidopsis thaliana C	5.9e+02
729	16	0.8	102074	31	AC011073	Human sapiens chromosome	5.9e+02
730	16	0.8	102074	31	AC011073	Human sapiens chromosome	5.9e+02
731	16	0.8	104778	34	AC005269	Drosophila melanogaster	5.9e+02
732	16	0.8	104710	21	AC002488	Human sapiens chromosome	5.9e+02
733	16	0.8	104951	31	AC004075	Human sapiens chromosome	5.9e+02
734	16	0.8	104951	31	AC004075	Human sapiens chromosome	5.9e+02
735	17	0.8	105232	31	HEB51R19	Human sapiens BAC95	5.9e+02
736	16	0.8	105984	33	AC005087	Human sapiens chromosome	5.9e+02
737	16	0.8	105984	33	HE43C13	Human sapiens chromosome	5.9e+02
738	16	0.8	106249	33	AC004464	Human sapiens chromosome	5.9e+02
739	16	0.8	106249	33	AC004464	Human sapiens chromosome	5.9e+02
740	16	0.8	106596	31	HUAC001661	Human sapiens chromosome	5.9e+02
741	16	0.8	107677	31	H44A0021	Human DNA sequence ***	5.9e+02
742	16	0.8	108564	33	HS074782	Human DNA sequence ***	5.9e+02
743	16	0.8	108564	33	HS074782	Human DNA sequence ***	5.9e+02
744	16	0.8	108975	31	AC004803	Human sapiens chromosome	5.9e+02
745	16	0.8	109013	33	HS59882	Human sapiens chromosome	5.9e+02
746	17	0.8	109155	31	HE10669	Human sapiens chromosome	5.9e+02
747	17	0.8	109155	31	HE10669	Human sapiens chromosome	5.9e+02
748	17	0.8	110000	33	CEH24810	Ctenophorabittia elegans	1.2e+02
749	17	0.8	110000	33	CEH24810	Ctenophorabittia elegans	1.2e+02
750	16	0.8	110057	39	GFY58825	Arabidopsis thaliana B	5.9e+02
751	16	0.8	110251	33	AC004493	Human sapiens chromosome	5.9e+02
752	16	0.8	110251	33	AC004493	Human sapiens chromosome	5.9e+02
753	16	0.8	111568	31	AP000025	Human sapiens genomic D	5.9e+02
754	16	0.8	111568	31	AC005125	Human sapiens chromosome	5.9e+02
755	16	0.8	111692	31	AC005162	Human sapiens BAC clone	5.9e+02
756	16	0.8	111692	31	AC005162	Human sapiens BAC clone	5.9e+02
757	16	0.8	112752	33	SC004161	Human sapiens chromosome	5.9e+02
758	16	0.8	112752	33	SC004161	Human sapiens chromosome	5.9e+02

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750	15	0.8	1130261	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
751	16	0.8	1130271	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
752	17	0.8	1130281	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
753	18	0.8	1130291	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
754	19	0.8	1130301	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
755	20	0.8	1130311	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
756	21	0.8	1130321	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
757	22	0.8	1130331	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
758	23	0.8	1130341	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
759	24	0.8	1130351	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
760	25	0.8	1130361	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
761	26	0.8	1130371	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
762	27	0.8	1130381	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
763	28	0.8	1130391	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
764	29	0.8	1130401	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
765	30	0.8	1130411	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
766	31	0.8	1130421	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
767	32	0.8	1130431	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
768	33	0.8	1130441	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
769	34	0.8	1130451	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
770	35	0.8	1130461	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
771	36	0.8	1130471	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
772	37	0.8	1130481	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
773	38	0.8	1130491	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
774	39	0.8	1130501	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
775	40	0.8	1130511	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
776	41	0.8	1130521	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
777	42	0.8	1130531	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
778	43	0.8	1130541	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
779	44	0.8	1130551	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
780	45	0.8	1130561	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
781	46	0.8	1130571	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
782	47	0.8	1130581	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
783	48	0.8	1130591	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
784	49	0.8	1130601	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
785	50	0.8	1130611	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
786	51	0.8	1130621	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
787	52	0.8	1130631	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
788	53	0.8	1130641	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
789	54	0.8	1130651	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
790	55	0.8	1130661	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
791	56	0.8	1130671	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
792	57	0.8	1130681	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
793	58	0.8	1130691	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
794	59	0.8	1130701	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
795	60	0.8	1130711	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
796	61	0.8	1130721	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
797	62	0.8	1130731	13	ATP6H11	Archoadopsis tholiana D	5.90e+02
798	63	0.8	1130741	13	ATP6H11	Ar	

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810	810	16	0.8	13.6568	13	AC004931	Homo sapiens clone D10	5.90e+02
811	811	16	0.8	13.6568	13	AC004931	Homo sapiens clone D10	5.90e+02
812	812	16	0.8	13.7111	21	H520723	Human DNA sequence ***	5.90e+02
813	813	16	0.8	13.7279	21	AC004860	Homo sapiens clone D20	5.90e+02
814	814	16	0.8	13.7361	11	AC004860	Homo sapiens clone RG210	5.90e+02
815	815	17	0.8	13.7368	11	AC004952	Homo sapiens clone D11	1.21e+02
816	816	17	0.8	13.7868	68	AC004952	Homo sapiens clone D11	1.21e+02
817	817	22	0.8	13.8187	22	MIM6461	Mus musculus Major Hla	5.90e+02
818	818	22	0.8	13.8187	22	MIM6461	Mus musculus Major Hla	5.90e+02
819	819	22	0.8	13.8945	21	AC004951	Homo sapiens DNA sequence	5.90e+02
820	820	17	0.8	13.9057	13	AC004951	*** SEQUENCING IN PROG	1.21e+02
821	821	16	0.8	13.9097	13	AC004591	*** SEQUENCING IN PROG	5.90e+02
822	822	16	0.8	13.9480	21	HAC002311	Homo sapiens Chromosome	5.90e+02
823	823	16	0.8	14.0000	11	AC004591	*** SEQUENCING IN PROG	5.90e+02
824	824	16	0.8	14.0000	11	AC004591	*** SEQUENCING IN PROG	5.90e+02
825	825	17	0.8	14.1131	13	H512929	Human DNA sequence ***	5.90e+02
826	826	17	0.8	14.1288	13	H513319	Human DNA sequence ***	1.21e+02
827	827	16	0.8	14.1301	13	H513319	Human DNA sequence ***	5.90e+02
828	828	16	0.8	14.2374	13	H513392	Homo sapiens clone D10	5.90e+02
829	829	16	0.8	14.2640	13	AC004936	Homo sapiens clone D10	5.90e+02
830	830	16	0.8	14.2761	13	H516665	Human DNA sequence ***	5.90e+02
831	831	16	0.8	14.2761	13	H516665	Human DNA sequence ***	5.90e+02
832	832	16	0.8	14.2761	14	AC004939	Drosophila melanogaster	1.21e+02
833	833	16	0.8	14.2761	14	AC004939	Drosophila melanogaster	1.21e+02
834	834	16	0.8	14.3310	13	AC005193	Homo sapiens clone D10	1.21e+02
835	835	16	0.8	14.3310	13	AC005193	Homo sapiens clone D10	1.21e+02
836	836	16	0.8	14.3310	13	AC005076	Homo sapiens clone RG2	5.90e+02
837	837	16	0.8	14.3941	21	AC004931	Homo sapiens PAC clone	5.90e+02
838	838	16	0.8	14.3941	21	AC004931	Homo sapiens PAC clone	5.90e+02
839	839	16	0.8	14.4360	21	H515162	Human DNA sequence ***	1.21e+02
840	840	16	0.8	14.4360	21	H515162	Human DNA sequence ***	1.21e+02
841	841	16	0.8	14.4709	13	H5151824	Homo sapiens DNA sequence	5.90e+02
842	842	16	0.8	14.4709	13	AC004952	Homo sapiens clone D11	5.90e+02
843	843	17	0.8	14.5126	21	H5151824	Human DNA sequence ***	1.21e+02
844	844	17	0.8	14.5126	21	H5151824	Human DNA sequence ***	1.21e+02
845	845	16	0.8	14.5126	21	H5151824	Human DNA sequence ***	1.21e+02
846	846	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
847	847	17	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
848	848	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
849	849	17	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
850	850	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
851	851	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
852	852	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
853	853	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
854	854	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
855	855	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
856	856	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
857	857	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
858	858	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
859	859	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02
860	860	16	0.8	14.5913	21	AC004230	*** SEQUENCING IN PROG	5.90e+02

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861	16	0.8	157232	13	H6407717	
862	16	0.8	157248	13	AC002312	Human DNA sequence ***
863	16	0.8	157684	22	AC002131	Human Chromosome 15 pA
864	16	0.8	158886	21	AC004574	Homo sapiens X(25) BAC
865	16	0.8	159030	21	AC004574	Homo sapiens chromosome 21
866	16	0.8	160203	21	H0242553	Homo sapiens chromosome 21
867	16	0.8	160899	13	AC004569	Homo sapiens clone DJO
868	16	0.8	161475	13	H0242520	Homo sapiens DNA sequence
869	16	0.8	161479	13	AC004574	Homo sapiens chromosome 21
870	16	0.8	161709	13	AC004574	Homo sapiens chromosome 21
871	16	0.8	161836	21	AC005120	Homo sapiens chromosome 21
872	16	0.8	163847	13	AC004581	Homo sapiens clone DJO
873	16	0.8	164049	13	AC005132	Homo sapiens clone DJO
874	16	0.8	164058	13	AC005132	Homo sapiens clone DJO
875	17	0.8	164675	13	AC004184	Homo sapiens clone DJO
876	17	0.8	165608	13	AC005088	Homo sapiens BAC clone
877	17	0.8	165609	13	AC005088	Homo sapiens BAC clone
878	16	0.8	165819	11	H0230104	Human NCIC clone R00449
879	16	0.8	165819	11	H0230104	Human Chromosome X clone
880	17	0.8	167564	13	CE156625	Ceomorphidus elegans
881	16	0.8	170000	13	AC004053	Human PAC clone
882	17	0.8	170136	21	AC003982	Human BAC clone R00111
883	17	0.8	170136	21	AC003982	Human Chromosome 21 pA
884	17	0.8	171789	13	H02402099	Homo sapiens Chromosome 13
885	16	0.8	171799	21	H15193182	Human DNA sequence ***
886	17	0.8	173902	22	AC002324	Human BAC clone R00111
887	17	0.8	173902	22	AC002324	Human BAC clone R00111
888	16	0.8	173909	22	AC002324	Human BAC clone R00111
889	17	0.8	173909	22	AC002324	Human BAC clone R00111
890	17	0.8	173915	21	H53AC000114	Human DNA sequence ***
891	16	0.8	173265	13	H372E16	Human DNA sequence ***
892	16	0.8	173457	21	AC003013	Human PAC clone DJO205
893	17	0.8	174630	13	H0230103	Human DNA sequence ***
894	16	0.8	174630	13	H0230103	Human DNA sequence ***
895	16	0.8	173766	13	AC004049	Homo sapiens chromosome 13
896	17	0.8	173766	13	AC004049	Homo sapiens chromosome 13
897	17	0.8	174731	14	AC004758	Drosophila melanogaster
898	17	0.8	174731	14	AC004758	Homo sapiens XQ8 gene
899	17	0.8	174731	14	AC004758	Homo sapiens XQ8 gene
900	17	0.8	174731	14	AC004758	Homo sapiens XQ8 gene
901	17	0.8	176791	13	AC002589	Human DNA sequence ***
902	17	0.8	176791	13	AC002589	Human DNA sequence ***
903	16	0.8	177142	21	AC004582	Human Chromosome 11p14
904	16	0.8	177142	21	AC004582	Human Chromosome X clone
905	16	0.8	177142	21	AC004582	Human Chromosome X clone
906	16	0.8	177902	13	CE156625	Ceomorphidus elegans
907	16	0.8	177902	13	CE156625	Ceomorphidus elegans
908	16	0.8	177923	27	U94848	Vaccinia virus strain
909	16	0.8	177923	27	U94848	Vaccinia virus strain
910	16	0.8	179246	13	AC004854	Homo sapiens clone DJO
911	16	0.8	179246	13	AC004854	Homo sapiens clone DJO
912	16	0.8	179319	13	AC005282	Homo sapiens clone DJO
913	16	0.8	179319	13	AC005282	Homo sapiens clone DJO
914	16	0.8	179913	13	AC005048	Homo sapiens clone R00
915	16	0.8	180114	13	H552D1	Human DNA sequence ***
916	16	0.8	180114	13	H552D1	Human DNA sequence ***
917	16	0.8	180133	13	AC004933	Homo sapiens clone DJO
918	16	0.8	180133	13	AC004933	Homo sapiens clone DJO

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912	17	0.8	183795	19	YBP12R	<i>Arabidopsis thaliana</i> C
913	17	0.8	183796	19	YBP12R	<i>Arabidopsis thaliana</i> C
914	16	0.8	184130	21	AC005209	Human sapiens chromosome
915	16	0.8	184949	21	AC005209	Human sapiens chromosome
916	16	0.8	185711	13	AC005216	Human sapiens BAC clone
917	16	0.8	185713	13	AC005216	Human sapiens BAC clone
918	16	0.8	185716	21	VC025H18	Human sapiens BAC clone
919	17	0.8	185717	21	VC025H18	Human sapiens BAC clone
920	16	0.8	185718	21	VC025H18	Human sapiens BAC clone
921	16	0.8	185719	21	VC025H18	Human sapiens BAC clone
922	17	0.8	185721	21	VC025H18	Human sapiens BAC clone
923	16	0.8	185722	21	VC025H18	Human sapiens BAC clone
924	16	0.8	185723	21	VC025H18	Human sapiens BAC clone
925	16	0.8	185724	21	VC025H18	Human sapiens BAC clone
926	16	0.8	185725	21	VC025H18	Human sapiens BAC clone
927	16	0.8	185726	21	VC025H18	Human sapiens BAC clone
928	17	0.8	185727	21	VC025H18	Human sapiens BAC clone
929	16	0.8	185728	21	VC025H18	Human sapiens BAC clone
930	16	0.8	185729	21	VC025H18	Human sapiens BAC clone
931	17	0.8	185730	21	VC025H18	Human sapiens BAC clone
932	16	0.8	185731	21	VC025H18	Human sapiens BAC clone
933	16	0.8	185732	21	VC025H18	Human sapiens BAC clone
934	16	0.8	185733	21	VC025H18	Human sapiens BAC clone
935	16	0.8	185734	21	VC025H18	Human sapiens BAC clone
936	17	0.8	185735	13	HC47384	Human sapiens DNA
937	17	0.8	187199	13	AC005054	Human sapiens clone RGO
938	16	0.8	187273	21	AC002464	Human BAC clone RG2041
939	16	0.8	187275	21	AC002464	Human BAC clone RG2041
940	17	0.8	189060	13	AC004831	Human sapiens chromosome
941	16	0.8	189101	22	MA0200665	Mouse musculus TCR beta
942	16	0.8	189704	13	HS526114	Human DNA sequence
943	17	0.8	190000	13	AC005614	Human sapiens clone NHO
944	17	0.8	190001	13	AC005614	Human sapiens clone NHO
945	16	0.8	190002	13	AC005614	Human sapiens clone NHO
946	16	0.8	200000	13	AC004670	Human sapiens clone RGO
947	16	0.8	200001	13	AC004670	Human sapiens clone RGO
948	16	0.8	200002	13	ATFC6A	<i>Arabidopsis thaliana</i> D
949	16	0.8	200164	22	HC0023987	Mouse musculus major histocompatibility complex class II A
950	16	0.8	200165	22	HC0023987	Mouse musculus major histocompatibility complex class II A
951	16	0.8	200204	21	H04007149	Human Chromosome 16 RA
952	16	0.8	202249	13	AC005376	*** SEQUENCING IN PROG
953	16	0.8	202249	13	AC005386	*** SEQUENCING IN PROG
954	16	0.8	202251	13	AC005224	Human sapiens XP22 BAC
955	17	0.8	203583	13	AC004940	Human sapiens clone DJO
956	17	0.8	203583	13	AC004940	Human sapiens clone DJO
957	17	0.8	203583	13	AC004940	Human sapiens clone DJO
958	17	0.8	203583	13	AC004940	Human sapiens clone DJO
959	16	0.8	203583	13	AC004940	Human sapiens clone DJO
960	16	0.8	203583	13	AC004940	Human sapiens clone DJO
961	16	0.8	203583	13	AC004940	Human sapiens clone DJO
962	16	0.8	203583	13	AC004940	Human sapiens clone DJO
963	16	0.8	203583	13	AC004940	Human sapiens clone DJO
964	16	0.8	203583	13	AC004940	Human sapiens clone DJO
965	16	0.8	203583	13	AC004940	Human sapiens clone DJO
966	16	0.8	203583	13	AC004940	Human sapiens clone DJO
967	16	0.8	203583	13	AC004940	Human sapiens clone DJO
968	16	0.8	203583	13	AC004940	Human sapiens clone DJO
969	16	0.8	203583	13	AC004940	Human sapiens clone DJO
970	16	0.8	203583	13	AC004940	Human sapiens clone DJO
971	16	0.8	203583	13	AC004940	Human sapiens clone DJO
972	16	0.8	203583	13	AC004940	Human sapiens clone DJO
973	16	0.8	203583	13	AC004940	Human sapiens clone DJO
974	16	0.8	203583	13	AC004940	Human sapiens clone DJO
975	16	0.8	203583	13	AC004940	Human sapiens clone DJO
976	16	0.8	203583	13	AC004940	Human sapiens clone DJO
977	16	0.8	203583	13	AC004940	Human sapiens clone DJO
978	16	0.8	203583	13	AC004940	Human sapiens clone DJO
979	16	0.8	203583	13	AC004940	Human sapiens clone DJO
980	16	0.8	203583	13	AC004940	Human sapiens clone DJO
981	16	0.8	203583	13	AC004940	Human sapiens clone DJO
982	16	0.8	203583	13	AC004940	Human sapiens clone DJO
983	16	0.8	203583	13	AC004940	Human sapiens clone DJO
984	16	0.8	203583	13	AC004940	Human sapiens clone DJO
985	16	0.8	203583	13	AC004940	Human sapiens clone DJO
986	16	0.8	203583	13	AC004940	Human sapiens clone DJO
987	16	0.8	203583	13	AC004940	Human sapiens clone DJO
988	16	0.8	203583	13	AC004940	Human sapiens clone DJO
989	16	0.8	203583	13	AC004940	Human sapiens clone DJO
990	16	0.8	203583	13	AC004940	Human sapiens clone DJO
991	16	0.8	203583	13	AC004940	Human sapiens clone DJO
992	16	0.8	203583	13	AC004940	Human sapiens clone DJO
993	16	0.8	203583	13	AC004940	Human sapiens clone DJO
994	16	0.8	203583	13	AC004940	Human sapiens clone DJO
995	16	0.8	203583	13	AC004940	Human sapiens clone DJO
996	16	0.8	203583	13	AC004940	Human sapiens clone DJO
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[illegible]

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ORGANISM      Homo sapiens.
Eukaryota:   mitochondrial eukaryotes: Metazoa: Chordata:
Vertebrata:  Mammalia: Eutheria: Primates: Catarrhini: Hominoidea:
Homo         Homo sapiens 1 (198902)
REFERENCE     Wilkerson, J.
JOURNAL       Direct Submission
Submitted (04-AUG-1997)  Chromosome X project Group
Submitted (04-AUG-1997)  Sanger, Centre, Hinxton,
Cambridge, England, UK
IMPORTAN:    ac.uk Clone requests: clones@qwanter.ac.uk
COMMENT      This sequence is the entire insert of clone 128N22.
              During sequence assembly data is compared from overlapping clones
              and differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the variations
              annotated may not be found in the sequence submission corresponding
              to the overlapping clone as we submit sequences with only a small
              overlap
              as described above.
              data was generated from part of bacterial clone contigs of
              human chromosomes constructed by the Sanger Centre Chromosome X
              mapping group. Further information can be found at
              http://www.sanger.ac.uk/HGP/ChrX/
              This sequence has been finished according to sequence map criteria
              and is therefore of high quality. It is not necessarily without
              such as compressions and repeats but not necessarily within known
              annotated human repeat sequence elements (e.g. Alu). Where the
              sequence is ambiguous, there is an annotation using the 'unsure'
              feature key. If end of clone 128N22 is at 1 in this sequence. The
              true right end of clone 128N22 is at 9901.
              128N22 is from the library RPCL1 constructed at the Roswell Park
              Cancer by the group of Peter de Jong
              For further details see http://hacpac.med.buffalo.edu/.
              Location/Qualifiers
                i. 98902      "Homo sapiens"
                  dbxref="taxon:9606"
                  /chromosome="X"
                  /map=Xq25-Xq26.3"
                  /clone="128N22"
                  /rpt="RPCL1"
                  5537..5891
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              repeat_region 5894..6027 repeat: matches 140. 1 of consensus"
              repeat_region 6028..7596 repeat: matches 140. 1 of consensus"
              /note="THE1B-INTERNAL repeat: matches 1980. 1 of

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[illegible]

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7597, 7857
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repeat_region
1128, .11463
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/notes-MIR2 repeat: matches 64, .146 of consensus"
repeat_region
1374, .16271
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repeat_region
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repeat_region
13703, .20202
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repeat_region
20300, .20438
/notes-MIR1 repeat: matches 139, .1 of consensus"
repeat_region
21333, .24552
/notes-MIR1 repeat: matches 426, .188 of consensus"
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24552, .24971
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25583, .25602
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repeat_region
/notes-10 copies of 4 mer 100 % conserved"
repeat_region
25669, .27057
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27355, .27743
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27961, .29977
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28961, .29977
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31789, .32008
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34586, .35060
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35205, .35404
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repeat_region
35881, .35929
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37480, .37776
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repeat_region
38408, .38882
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41458, .41558
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repeat_region 59876..60291
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repeat_region 60151..60518
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repeat_region 62376..62700
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repeat_region 62577..62700
/note="MIR repeat: matches 155..1 of consensus"
repeat_region 62958..63116
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repeat_region 65252..65291
/note="MIR repeat: matches 358..498 of consensus"
repeat_region 66954..67477
/note="MIR repeat: matches 54..568 of consensus"
repeat_region 67604..67785
/note="MIR repeat: matches 248..49 of consensus"
repeat_region 70699..70857
/note="MIR repeat: matches 145..1 of consensus"
repeat_region 71857..72186
/note="MIR repeat: matches 559..902 of consensus"
repeat_region 72007..72186
/note="MIR repeat: matches 473..920 of consensus"
repeat_region 76946..77246
/note="ALUSG repeat: matches 1..300 of consensus"
repeat_region 81475..81736

KEYWORDS HTG: HTGS_PHASE1.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE 1 (bases 1 to 177455)
AUTHORS Waterston.R.H.
TITLE The sequence of Homo sapiens clone
REFERENCE 2 (bases 1 to 177455)
AUTHORS Waterston.R.H.
TITLE Direct submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
NO 63108, USA

*** WARNING: Phase 1 High Throughput Genome Sequence ***
This sequence is unfinished. It consists of 23 contigs for which the order is not known; their order in this record is arbitrary. In some cases, the exact lengths of the gaps between the contigs are also unknown; these gaps are presented as the run of 'N' at a convenient only. When sequencing is complete, the gaps will be filled in. The sequence is presented as a single finished sequence with the same accession number.
1 6750: contig of 6750 bp in length
6751 6765: gap of unknown length
13005 13139: gap of unknown length
13220 19546: contig of 6327 bp in length
19547 19561: gap of unknown length
22132 22140: contig of 2589 bp in length
22146 24552: contig of 2407 bp in length
24553 24567: gap of unknown length
24568 28336: contig of 3769 bp in length
28337 30311: gap of unknown length
30312 30326: gap of unknown length
30327 32436: contig of 2110 bp in length
32437 34081: gap of unknown length
34082 38098: gap of unknown length
38099 40759: contig of 2661 bp in length
40760 40774: gap of unknown length
40775 44626: gap of unknown length
44627 47261: contig of 2635 bp in length
47262 47276: gap of unknown length
47277 71759: contig of 24482 bp in length
71760 71773: gap of unknown length

71774 85598: contig of 13825 bp in length
85599 85613: gap of unknown length
85614 87745: contig of 2132 bp in length
87746 87760: gap of unknown length
87761 91632: gap of unknown length
91633 91646: gap of unknown length
91647 105068: contig of 13422 bp in length
105069 105083: gap of unknown length
105084 118545: contig of 13862 bp in length
118546 118560: gap of unknown length
118561 122979: contig of 4018 bp in length
122980 122993: gap of unknown length
122994 126445: contig of 3452 bp in length
126446 126460: gap of unknown length
126461 144187: contig of 18127 bp in length
144188 144802: gap of unknown length
144803 156913: contig of 12111 bp in length
156914 156928: gap of unknown length
156929 156943: contig of 20237 bp in length.
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/db_xref="taxon:9606"
/db_xref="clone:9606"
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Best Local Similarity 100.0%: Pct 100, DP 13, Length 177455;
Matches 20, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
Db 30742 GCCAGATTAGGACCATCC 30761
Cp 1516 GCCAGATTAGGACCATCC 1497
RESULT 16 G05059 274 bp DNA STS 19-OCT-1995
LOCUS G05059
DEFINITION human STS WI-6458.
ACCESSION G05059
KEYWORDS
MID 9722017
SOURCE
Homo sapiens
Homo sapiens genome wide STS created from sheared whole human DNA.
ORGANISM
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Mammalia; Primates; Hominidae; Theria; Eutheria; Archonta; Placentalia;
Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 274)
AUTHORS Hudson.T.
TITLE Whitehead Institute/MIT Center for Genome Research; Random Genome


```

US-08-461-011a-1.1ye

JOURNAL Plant Mol. Biol. 33 (2), 223-234 (1997)
MEDLINE 97189556
REFERENCE 2 (bases 1 to 780)
AUTHORS Van Damme, E. J. M. and Van Damme, E. J. M.
TITLE Amino acid sequence of the mannose-specific lectin from
JOURNAL Leuven, Lab Phytopathology and Plant Protection, Willem de Croylaan
42, Leuven Heverlee, Brabant, Belgium, 3001
FEATURES
Source
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/cisname="type" roots"
1. 7
8. .553
/citation="(1)
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/codon_end="end"
/product="mannose-specific lectin"
/DB_xref="PI:D:G1840049"
/translation="MGRITSPFAMRITATVAITLTASTCHARNVYINSGLTAGQ
SRIETKRDQDQKVALYETSPFAMRITGQKAGHARNDGDFEYVDVNGSP
SRIETKRDQDQKVALYETSPFAMRITGQKAGHARNDGDFEYVDVNGSP
GGPVVNYNTVAETKVGGA"
8. .97
sig_peptide
mat_peptide
8. .529
product="lectin"
1/UTR
mat_peptide
209 a 152 c 198 g 221 t
BASE COUNT
ORIGIN
Query Match 0.94; Score 19; DB 19; Length 780;
Identity 100.0%; Pos. 1-780; Mismatches 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 36 CANTAGATGAGATAGCCAC 54
Cp 588 CANTAGATGAGATAGCCAC 570

RESULT 25 BREGGILCO 835 bp mRNA VRL 13-OCT-1993
LOCUS BREGGILCO 835 bp mRNA
SOURCE BREGGILCO, respiratory syncytial virus G glycoprotein mRNA.
ACCESSION U0470
KEYWORDS 1947680
NID 9407680
KEYWORDS G glycoprotein.
SOURCE Ovine respiratory syncytial virus cDNA to mRNA.
ORIGIN
BREGGILCO, respiratory syncytial virus G glycoprotein.
Paramyxoviridae; Paramyxovirus.

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US-08-466-011h-1.fye

The Nov 24 08:10:56 1998

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FYTEKIGDRLVLTQINDTAQGRSGLGVAFYAGDGLQVDYVNMSFDNDIM
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LWIKRHHKRNKPKKIPFNISFTIISGNC
BASE COUNT      288 a   174 c   234 g   257 t
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Query Match          0.94; Score 18; DB 19; Length 993;
Local similarity 0.94; Score 18; DB 19; Length 993;
Match 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    269 TATAGAGGACGATTCT 286
      |||||iiiiiii|||||
Qy    188 TATAGAGGCGATTCT 205

RESULT 27 RANCW2       1057 bp     DNA           MM      01-DEC-1997
LOCUS   Oryctolagus cuniculus collagenase-1 precursor (MMP-1) gene, exon
DEFINITION 2, 3 and 4.
ACCESSION M17821
VERSION 1
KEYWORDS  g164893
SOURCE   2 of 5
ORGANISM Oryctolagus cuniculus.
          Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
          Lagomorphs; Leporidae; Oryctolagus.
REFERENCE Finl.M.E., Gross.R.H. and Brinckerhoff,C.E.
AUTHORS Characterization of rabbit genes for synovial cell collagenase
JOURNAL Arthritis Rheum. 39 (11), 1301-1315 (1996)
MEDLINE 27049899
PMID     8749899
REFERENCE Finl.M.E., Plucinskis,I.M., Mayer,A.S., Gross,R.H. and
AUTHORS Brinckerhoff,C.E.
TITLE A gene for rabbit synovial cell collagenase: member of a family of
JOURNAL metalloproteinases that degrade the connective tissue matrix
MEDLINE 88077876
PMID     88077876
REFERENCE Vincenzi,M.P., Coon,C.I., White,L.A., Barchowsky,A. and
AUTHORS Interleukin-1-stimulated transcriptional activation of
the interstitial collagenase genes, MMP-1, in
interleukin-1-stimulated synovial fibroblasts
JOURNAL Arthritis Rheum. 39 (4), 574-582 (1996)
MEDLINE 8749899
PMID     8749899
REFERENCE Finl.M.E., Gross.R.H. and Brinckerhoff,C.E.
AUTHORS Interleukin-1-stimulated transcriptional activation of
the interstitial collagenase genes, MMP-1, in
interleukin-1-stimulated synovial fibroblasts
JOURNAL Arthritis Rheum. 39 (4), 574-582 (1996)
MEDLINE 8749899
PMID     8749899
REFERENCE Finl.M.E., Gross.R.H. and Brinckerhoff,C.E.
AUTHORS Interleukin-1-stimulated transcriptional activation of
the interstitial collagenase genes, MMP-1, in
interleukin-1-stimulated synovial fibroblasts
JOURNAL Arthritis Rheum. 39 (4), 574-582 (1996)
MEDLINE 8749899
PMID     8749899

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RESULT 28 QM40666 1178 bp mRNA PIN 28-AUG-1997
LOCUS Glycine max biotin carboxyl carrier protein precursor (accb-1)
DEFINITION
ACCESSION QM40666
KEYWORDS complete cds.
NID g1143318
SOURCE soybean
ORGANISM Glycine max
CHARACTERISTICS: Mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; vascular plants; seed
plants; Magnoliophyta; Magnoliopsida; Rutanae; Sapindales;
Fabaceae; Leguminosae; Glycine.
REFERENCE
AUTHORS Reverdatto,S.V., Bellinson,V. and Nielsen,M.C.
TITLE Characterization of a cDNA clone encoding a BCCP subunit of
acetyl-CoA carboxylase from soybean (Accession No.
U01484)
JOURNAL Plant Physiol. 111, 652 (1996)
REFERENCE
AUTHORS Nielsen,M.C., Reverdatto,S.V. and Bellinson,V.A.
TITLE Glycine max biotin carboxyl carrier protein precursor
JOURNAL Plant Physiol. 111, 652 (1996)
FEATURES
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/db_xref="taxon:3847"
gene 1..1178
/gene="accb-1"
transit_peptide 1..1178
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/note="Cleavage site position determined by sequencing of
N-terminus of mature peptide, produced during chloroplast
import of radiolabelled precursor; precursor was generated
in vitro transcription-translation
/evidence="experimental"
CDS 109..897
/gene="accb-1"
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/note="Biotin-containing enzyme catalyzing ATP-dependent
malonyl-CoA formation, a first committed step in the de
novo biosynthesis of fatty acids. Localised acetyl-CoA
carboxylase (prokaryotic type); precursor produced in
vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
/codon_start=1
/product="biotin carboxyl carrier protein precursor"

JOURNAL Submitted (27-FEB-1997) E. Rao, Institut fuer Humangenetik, INF
328, 68120 Heidelberg, FRG
FEATURES
source 1..1178
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malonyl-CoA formation, a first committed step in the de
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carboxylase (prokaryotic type); precursor produced in
vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
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carboxylase (prokaryotic type); precursor produced in
vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
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misc_feature 440..519
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 321 ATGACGAGGAGAACTCA 338
QY 1712 ATGACGAGGAGAACTCA 1729
RESULT 30 HSHROXA 1891 bp RNA
LOCUS H. sapiens mRNA for SHOX gene.
DEFINITION H. sapiens mRNA for SHOX protein.
ACCESSION U11536
KEYWORDS SHOX gene.
SOURCE human.
ORGANISM Homo sapiens
CHARACTERISTICS: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-1997) Medicine, Dartmouth Medical School, 508
Vail Building, Hanover, NH 03755, USA
REFERENCE
AUTHORS Vincent,M.P., Coon,C.I., White,L.A., Barchowsky,A. and
Brinckerhoff,C.E.
TITLE Direct Submission
JOURNAL Medicine, Dartmouth Medical School, 508
Vail Building, Hanover, NH 03755, USA
REMARK Sequence update by submitter
FEATURES
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/db_xref="taxon:3847"
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malonyl-CoA formation, a first committed step in the de
novo biosynthesis of fatty acids. Localised acetyl-CoA
carboxylase (prokaryotic type); precursor produced in
vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
/codon_start=1
/product="biotin carboxyl carrier protein precursor"
CDS 109..897
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vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
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QY 63 CTGCTTCTCTACGCC 80

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carboxylase (prokaryotic type); precursor produced in
vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 155 GCTCAGACACTCTCTCC 172
QY 1599 GCTCAGACACTCTCTCC 1515
RESULT 29 HSHROXA 1891 bp RNA
LOCUS H. sapiens mRNA for SHOX protein.
DEFINITION H. sapiens mRNA for SHOX protein.
ACCESSION U11535
KEYWORDS SHOX gene.
SOURCE human.
ORGANISM Homo sapiens
CHARACTERISTICS: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Vincent,M.P., Coon,C.I., White,L.A., Barchowsky,A. and
Brinckerhoff,C.E.
TITLE Direct Submission
JOURNAL Medicine, Dartmouth Medical School, 508
Vail Building, Hanover, NH 03755, USA
REMARK Sequence update by submitter
FEATURES
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malonyl-CoA formation, a first committed step in the de
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carboxylase (prokaryotic type); precursor produced in
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proteolytically processed by isolated chloroplasts"
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/note="Biotin-containing enzyme catalyzing ATP-dependent
malonyl-CoA formation, a first committed step in the de
novo biosynthesis of fatty acids. Localised acetyl-CoA
carboxylase (prokaryotic type); precursor produced in
vitro transcription-translation was imported and
proteolytically processed by isolated chloroplasts"
/codon_start=1
/product="biotin carboxyl carrier protein precursor"
misc_feature 440..519
/note="homodomain"
/note="homodomain"
BASE COUNT 303 a 224 c 234 g 296 t
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Query Match 0.94; Score 18; DB 15; Length 1057;
Best Local Similarity 100.0%; Pred. No. 2.23e+01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 399 CTGCTTCTCTACGCC 406
QY 63 CTGCTTCTCTACGCC 80

[illegible]

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Note: remainder of annotations omitted.

Query Match      DB 14: Length 34397;
Similarity 100%;   (New Genes=0)
Matches 18;         O: Mismatches 0; Indels 0; Gaps 0;

Db 251 GACTGACGACGACGAC 268
Cp 1202 GACTGACGACGACGAC 1185

RESULT 49 AC004700 37055 bp DNA PFI 19-MAY-1998
DEFINITION Homo sapiens chromosome 19, contig P14498, complete sequence.
ACCESSION AC004700
VERSION 1
KEYWORDS g3138891
MISC.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Lancardini J, O' McCready P M, Skowronski E, Adamson A W,
Burkhardt-Schultz K, Gordon L, Kyle A, Ramirez M, Stillewag S.,
Phan H, Velasco M, Bo L, Regala W., Terry A., Ganes J., Villa J.,
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Krauss R., Krawinkel A., Krawinkel A., Krawinkel A., Krawinkel A.
Sequence analysis of a 2.5 kb region in 19q13.2 containing a
clustered CXM/PSG gene family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 37055)
2 (bases 1 to 37055)
Direct Submission
JOURNAL
TITLE
COMMENT Submitted (19-MAY-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
AC004700 overlaps contig g36371 to the left and BAC 33851 to the
right. Additional chr 19 map and sequence information may be
obtained at: http://www.bio.tlnl.gov/abrp/genome/genome.html.
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Murinae; Mus.
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Lau, J. E., Thompson L.H., Montgomery M.A.,
Stilwagen S.A., Scheidecker L. and Tebb R.S.
TITLE Genomic sequence comparison of the human and mouse XRCCL1 DNA repair

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JOURNAL Genomics (1995) In press
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C	353	15	0	7	783	14	Q75428	Human A-1BB polypept	1.75e+02	C	404	15	0	7	1081	38	T56842	Intron 12 of human PR	6.90e+02
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C	355	14	0	7	791	34	T650484	Rat calbindin-D9K	6.90e+02	C	406	15	0	7	1080	22	T12305	Sardinian tomato yell	1.75e+02
C	356	15	0	7	791	34	T650484	Rat calbindin-D9K	6.90e+02	C	407	15	0	7	1080	22	T12305	Sardinian tomato yell	1.75e+02
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463	15	1359.14	GB8434	Human mclm77 clone	1.75e-02
464	14	1359.2	Q11843	Human leucoperoxidase	1.75e-02
465	14	1359.2	Q11843	Human leucoperoxidase	1.75e-02
466	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
467	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
468	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
469	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
470	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
471	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
472	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
473	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
474	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
475	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
476	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
477	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
478	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
479	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
480	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
481	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
482	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
483	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
484	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
485	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
486	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
487	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
488	13	1362.13	GA5079	Human glucokinase gene	6.90e-02
489	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
490	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
491	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
492	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
493	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
494	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
495	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
496	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
497	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
498	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
499	14	1362.13	GA5079	Human glucokinase gene	6.90e-02
500	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
501	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
502	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
503	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
504	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
505	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
506	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
507	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
508	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
509	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
510	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
511	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
512	15	1362.13	GA5079	Human glucokinase gene	6.90e-02
513	15	1362.13			

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C 961	15	0.7	13104.2	0.46852	Clone of recombinant	1.75e+02
C 962	15	0.7	13144.2	0.41288	P-dentificans genes	1.75e+02
C 963	14	0.7	14114.1	0.71321	Plasmodium PBO50 encodino	6.90e+02
C 964	14	0.7	14114.1	0.71321	Plasmodium PBO50 encodino	6.90e+02
C 965	14	0.7	14507.32	0.73568	Expression augmenting	6.90e+02
C 966	14	0.7	15155.3	0.85017	DNA encoding Factor-V	6.90e+02
C 967	14	0.7	15338.3	0.81139	HPIA2-8 gene.	6.90e+02
C 968	14	0.7	15338.3	0.81139	Human PflNcG11 expr	6.90e+02
C 969	14	0.7	15351.38	0.74055	Genomic DNA of human	6.90e+02
C 970	14	0.7	17041.3	0.321065	Genomic DNA of human	6.90e+02
C 971	14	0.7	17041.32	0.67057	PACPAF2-8 DNA.	6.90e+02
C 972	14	0.7	17350.32	0.72708	HOPI human otaogenic	6.90e+02
C 973	14	0.7	17350.32	0.72708	HOPI human otaogenic prot	6.90e+02
C 974	14	0.7	17415.17	0.711659	Human otaogenic prot	6.90e+02
C 975	14	0.7	18012.6	0.63952	HSA genes.	6.90e+02
C 976	14	0.7	18124.32	0.72882	Plasmodium var-7 gene	6.90e+02
C 977	14	0.7	20303.1	0.716599	Human deoxyxynyl-glyc	6.90e+02
C 978	14	0.7	20303.1	0.716599	Human deoxyxynyl-glyc	6.90e+02
C 979	14	0.7	24593.3	0.850236	Sequences of Opine syn	6.90e+02
C 980	14	0.7	24596.3	0.850162	Complete nucleotide s	6.90e+02
C 981	14	0.7	24596.3	0.850162	Complete nucleotide s	6.90e+02
C 982	14	0.7	24700.1	0.750145	Mouse syndecan gene s	6.90e+02
C 983	14	0.7	24700.1	0.750145	Mouse syndecan gene s	6.90e+02
C 984	14	0.7	26784.31	0.716596	Human deoxyxynyl-glyc	6.90e+02
C 985	14	0.7	28994.39	0.15826	Genomic DNA for inter	6.90e+02
C 986	14	0.7	29544.7	0.712460	Ovine adenovirus geno	6.90e+02
C 987	14	0.7	30254.3	0.712460	Walpian largy subunit	6.90e+02
C 988	14	0.7	30254.3	0.712460	Walpian largy subunit	6.90e+02
C 989	14	0.7	30256.3	0.760557	Recombinant cis-actin	6.90e+02
C 990	14	0.7	35000.36	0.760557	Recombinant cis-actin	6.90e+02
C 991	14	0.7	35408.31	0.759272	Recombinant adenovirus	6.90e+02
C 992	14	0.7	35539.3	0.760558	Recombinant trans-act	6.90e+02
C 993	14	0.7	35539.3	0.760558	Recombinant trans-act	6.90e+02
C 994	14	0.7	43377.35	0.779508	Platenolide synthase	6.90e+02
C 995	14	0.7	53287.38	0.754111	L5 myoblastotriphage L5	1.75e+02
C 996	15	0.7	53287.38	0.754111	L5 myoblastotriphage L5	1.75e+02
C 997	14	0.7	53288.9	0.47357	Human PflI gene.	6.90e+02
C 998	14	0.7	53575.3	0.794102	AcNPV genomic DNA	6.90e+02
C 999	14	0.7	53575.3	0.794102	AcNPV genomic DNA	6.90e+02
C 1000	15	0.7	53889.17	0.713635	Mycoplasma genitalium	1.75e+02
C 1001	15	0.7	59007.37	0.758840	Mycoplasma genitalium	1.75e+02
C 1002	15	0.7	59007.37	0.758840	Mycoplasma genitalium	1.75e+02

ALIGNMENTS

RESULT	1	
ID	T59619	standard: cDNA; 2003 BP.
AC	T59619:	
DT	31-MAY-1997	(first entry)
DE	G-protein parathyroid hormone	receptor HLTGD74 cDNA.
DE	G-protein parathyroid hormone	receptor; HLTGD74; parathormone; PTH;
DE	calcium; signal transduction; agonist;	antagonist; hypocalcemia;
KW		

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US-08-468-011A-1.1mg

[illegible]

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[illegible]

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PS Example 2; Page 37; 62pp; English.
 CC A 5' PCR primer (T59622) contains a HindIII restriction site plus
 CC a sequence from the 5' untranslated region of the human G-protein
 CC receptor. The PCR product was incorporated into vector pCDNA3/amp
 CC to allow prodn. of recombinant HLTG74 (see also W12695) in
 CC transfected cells.
 SQ Sequence 27 BP; 4 A; 3 C; 10 G; 10 T;

Query Match 1.13; Score 22; DB 29; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.58e-03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gttggcattatggagcgttttt 22
 QY 20 ttggcattatggagcgttttt 41

RESULT
 ID T12244 standard; cDNA; 1514 BP.
 DE Human G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
 DE 08-APR-1996 (first entry)
 DE Rat CRF2-beta receptor; corticotropin-releasing factor-2 receptor;
 KW cerebrovascular disorder; memory disorder; Alzheimer disease;
 KW transgenic animal; ss.
 OS Rattus sp.
 FT Key
 FT cda 44..1339
 PT W09534651-A2 /tag= a
 PD 21-DEC-1995.
 PF 14-JUN-1995; 007757.
 PR 14-JUN-1994; US-259959.
 PR 07-JUN-1995; US-485984.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PI Chalmers D, De Souza EB, Grigoriadis DE, Liaw CW;
 PI Lovenberg TW, Oltersdorf T;
 PI P-858; R4057/05.
 DR Corticotropin-releasing factor-2 receptor, and DNA encoding it -
 PT used to isolate CRF-2 receptor antagonists for the treatment of
 PT cerebrovascular disorders, memory disorders and Alzheimer's disease
 CC A cDNA sequence (T12244) codes for rat corticotropin-releasing
 CC factor-2-beta (CRF2-beta) receptor (R90575), a G-coupled protein
 CC receptor involved in signal transduction. The cDNA is obtd. from a
 CC rat brain cDNA library using a probe (T12245) based on rat CRF2
 CC receptor cDNA. The cDNA can be used e.g. for the prodn. of recombinant

Query Match 1.13; Score 23; DB 17; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 2.44e-04;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1260 tctctcagggtttcttctgtc 1282
 QY 1296 tctctcagggtttcttctgtc 1318

RESULT
 ID T59624 standard; DNA; 38 BP.
 DE Human G-protein parathyroid hormone receptor; HLTG74 - used to
 DE identify (antagonists, used in the treatment of hypo- or
 DE G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
 DE 08-APR-1996 (first entry)
 DE Rat CRF2-alpha receptor cDNA.
 KW CRF2-alpha receptor; corticotropin-releasing factor-2 receptor;
 KW cerebrovascular disorder; memory disorder; Alzheimer disease;
 KW transgenic animal; ss.
 OS Rattus sp.
 FT Key
 FT cda 216..1452
 PT W09534651-A2 /tag= a
 PD 21-DEC-1995.
 PF 14-JUN-1995; 007757.
 PR 14-JUN-1994; US-259959.
 PR 07-JUN-1995; US-485984.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PI Chalmers D, De Souza EB, Grigoriadis DE, Liaw CW;
 PI Lovenberg TW, Oltersdorf T;
 PI P-858; R4057/05.
 DR Corticotropin-releasing factor-2 receptor, and DNA encoding it -
 PT used to isolate CRF-2 receptor antagonists for the treatment of
 PT cerebrovascular disorders, memory disorders and Alzheimer's disease
 CC A cDNA sequence (T59624) codes for rat corticotropin-releasing
 CC factor-2-alpha (CRF2-alpha) receptor (R90574), a G-coupled protein
 CC receptor involved in signal transduction. The cDNA is obtd. from a
 CC rat hypothalamus cDNA library using a probe (T12245) based on rat CRF2
 CC receptor cDNA. The cDNA can be used e.g. for the prodn. of recombinant
 CC CRF2 receptor in transgenic animals. The cDNA can be used e.g. for the
 CC prodn. of transgenic animals used to study the role of the receptor in
 CC metabolism.

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CC CRF2 receptor in host cells, in the prepn. of probes used to identify
 CC polymorphisms linked to the CRF2 receptor gene, and in the breeding
 CC of transgenic animals used to study the role of the receptor in
 SQ Sequence 1514 BP; 320 A; 474 C; 365 G; 355 T;

Query Match 1.13; Score 23; DB 17; Length 1514;
 Best Local Similarity 100.0%; Pred. No. 2.44e-04;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1148 tctctcagggtttcttctgtc 1170
 QY 1296 tctctcagggtttcttctgtc 1318

RESULT
 ID T12243 standard; cDNA; 1626 BP.
 DE Human G-protein parathyroid hormone receptor; HLTG74 5' PCR primer.
 DE 08-APR-1996 (first entry)
 DE Rat CRF2-alpha receptor cDNA.
 KW CRF2-alpha receptor; corticotropin-releasing factor-2 receptor;
 KW cerebrovascular disorder; memory disorder; Alzheimer disease;
 KW transgenic animal; ss.
 OS Rattus sp.
 FT Key
 FT cda 216..1452
 PT W09534651-A2 /tag= a
 PD 21-DEC-1995.
 PF 14-JUN-1995; 007757.
 PR 14-JUN-1994; US-259959.
 PR 07-JUN-1995; US-485984.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
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 PI P-858; R4057/05.
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 PT used to isolate CRF-2 receptor antagonists for the treatment of
 PT cerebrovascular disorders, memory disorders and Alzheimer's disease
 CC A cDNA sequence (T12243) codes for rat corticotropin-releasing
 CC factor-2-alpha (CRF2-alpha) receptor (R90574), a G-coupled protein
 CC receptor involved in signal transduction. The cDNA is obtd. from a
 CC rat hypothalamus cDNA library using a probe (T12245) based on rat CRF2
 CC receptor cDNA. The cDNA can be used e.g. for the prodn. of recombinant
 CC CRF2 receptor in transgenic animals. The cDNA can be used e.g. for the
 CC prodn. of transgenic animals used to study the role of the receptor in
 CC metabolism.

Tue Nov 24 08:10:57 1998 US-08-468-011A-1.rmg

PS Example 2; Page 37; 62pp; English.
 CC A 5' PCR primer (T59622) contains a HindIII restriction site plus
 CC a sequence from the 5' untranslated region of the human G-protein
 CC receptor. The PCR product was incorporated into vector pCDNA3/amp
 CC to allow prodn. of recombinant HLTG74 (see also W12695) in
 CC transfected cells.
 SQ Sequence 27 BP; 4 A; 3 C; 10 G; 10 T;

Query Match 1.13; Score 22; DB 29; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.58e-03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gttggcattatggagcgttttt 22
 QY 20 ttggcattatggagcgttttt 41

RESULT
 ID T12244 standard; cDNA; 1514 BP.
 DE Human G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
 DE 08-APR-1996 (first entry)
 DE Rat CRF2-beta receptor; corticotropin-releasing factor-2 receptor;
 KW cerebrovascular disorder; memory disorder; Alzheimer disease;
 KW transgenic animal; ss.
 OS Rattus sp.
 FT Key
 FT cda 44..1339
 PT W09534651-A2 /tag= a
 PD 21-DEC-1995.
 PF 14-JUN-1995; 007757.
 PR 14-JUN-1994; US-259959.
 PR 07-JUN-1995; US-485984.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PI Chalmers D, De Souza EB, Grigoriadis DE, Liaw CW;
 PI Lovenberg TW, Oltersdorf T;
 PI P-858; R4057/05.
 DR Corticotropin-releasing factor-2 receptor, and DNA encoding it -
 PT used to isolate CRF-2 receptor antagonists for the treatment of
 PT cerebrovascular disorders, memory disorders and Alzheimer's disease
 CC A cDNA sequence (T12244) codes for rat corticotropin-releasing
 CC factor-2-beta (CRF2-beta) receptor (R90575), a G-coupled protein
 CC receptor involved in signal transduction. The cDNA is obtd. from a
 CC rat brain cDNA library using a probe (T12245) based on rat CRF2
 CC receptor cDNA. The cDNA can be used e.g. for the prodn. of recombinant

Query Match 1.13; Score 23; DB 17; Length 1626;
 Best Local Similarity 100.0%; Pred. No. 2.44e-04;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1260 tctctcagggtttcttctgtc 1282
 QY 1296 tctctcagggtttcttctgtc 1318

RESULT
 ID T59624 standard; DNA; 38 BP.
 DE Human G-protein parathyroid hormone receptor; HLTG74 - used to
 DE identify (antagonists, used in the treatment of hypo- or
 DE G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
 DE 08-APR-1996 (first entry)
 DE Rat CRF2-alpha receptor cDNA.
 KW CRF2-alpha receptor; corticotropin-releasing factor-2 receptor;
 KW cerebrovascular disorder; memory disorder; Alzheimer disease;
 KW transgenic animal; ss.
 OS Rattus sp.
 FT Key
 FT cda 216..1452
 PT W09534651-A2 /tag= a
 PD 21-DEC-1995.
 PF 14-JUN-1995; 007757.
 PR 14-JUN-1994; US-259959.
 PR 07-JUN-1995; US-485984.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PI Chalmers D, De Souza EB, Grigoriadis DE, Liaw CW;
 PI Lovenberg TW, Oltersdorf T;
 PI P-858; R4057/05.
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 PT used to isolate CRF-2 receptor antagonists for the treatment of
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 CC factor-2-alpha (CRF2-alpha) receptor (R90574), a G-coupled protein
 CC receptor involved in signal transduction. The cDNA is obtd. from a
 CC rat hypothalamus cDNA library using a probe (T12245) based on rat CRF2
 CC receptor cDNA. The cDNA can be used e.g. for the prodn. of recombinant
 CC CRF2 receptor in transgenic animals. The cDNA can be used e.g. for the
 CC prodn. of transgenic animals used to study the role of the receptor in
 CC metabolism.

Tue Nov 24 08:10:57 1998 US-08-468-011A-1.rmg

CC CRF2 receptor in host cells, in the prepn. of probes used to identify
 CC polymorphisms linked to the CRF2 receptor gene, and in the breeding
 CC of transgenic animals used to study the role of the receptor in
 SQ Sequence 1514 BP; 320 A; 474 C; 365 G; 355 T;

Query Match 1.13; Score 23; DB 17; Length 1514;
 Best Local Similarity 100.0%; Pred. No. 2.44e-04;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1148 tctctcagggtttcttctgtc 1170
 QY 1296 tctctcagggtttcttctgtc 1318

RESULT
 ID T12243 standard; cDNA; 1626 BP.
 DE Human G-protein parathyroid hormone receptor; HLTG74 5' PCR primer.
 DE 08-APR-1996 (first entry)
 DE Rat CRF2-alpha receptor cDNA.
 KW CRF2-alpha receptor; corticotropin-releasing factor-2 receptor;
 KW cerebrovascular disorder; memory disorder; Alzheimer disease;
 KW transgenic animal; ss.
 OS Rattus sp.
 FT Key
 FT cda 216..1452
 PT W09534651-A2 /tag= a
 PD 21-DEC-1995.
 PF 14-JUN-1995; 007757.
 PR 14-JUN-1994; US-259959.
 PR 07-JUN-1995; US-485984.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PI Chalmers D, De Souza EB, Grigoriadis DE, Liaw CW;
 PI Lovenberg TW, Oltersdorf T;
 PI P-858; R4057/05.
 DR Corticotropin-releasing factor-2 receptor, and DNA encoding it -
 PT used to isolate CRF-2 receptor antagonists for the treatment of
 PT cerebrovascular disorders, memory disorders and Alzheimer's disease
 CC A cDNA sequence (T12243) codes for rat corticotropin-releasing
 CC factor-2-alpha (CRF2-alpha) receptor (R90574), a G-coupled protein
 CC receptor involved in signal transduction. The cDNA is obtd. from a
 CC rat hypothalamus cDNA library using a probe (T12245) based on rat CRF2
 CC receptor cDNA. The cDNA can be used e.g. for the prodn. of recombinant
 CC CRF2 receptor in transgenic animals. The cDNA can be used e.g. for the
 CC prodn. of transgenic animals used to study the role of the receptor in
 CC metabolism.

QY 89 CATGGCTGGCTGGGGC 106

RESULT 6
ID 07473 standard: DNA: 339 BP.
AC 07473:
DT 23-SEP-1994 (first entry)
DE Human genome fragment (Preferred)
KW detection: homology: human; adrenal tissue; da.
OS Homo sapiens.
PN W09401548-A.
PR 13-JUL-1994: G01467.
PP 13-JUL-1994: GB-01467.
PA (MED-) MEDICAL RES COUNCIL.
PI Gross J, Hadfield RM, Howells D, Kelly M, Shaw D;
DR wp1: 94-0310565/04.
DE New nucleic acid fragment encoding gene products - can be used
PT for genetic analysis and mapping
PS Claim 1: Page 544; 61pp; English.
CC This is a full-length cDNA sequence of the human adrenomedullary
CC the placenta or bone marrow comprising of (A), sequence
CC selected from (076401-077613), (B) an allelic variation of a
CC sequence as described in (A), or (C) a sequence complementary
CC to (A) or (B).
CC The sequences exhibit no more than 90% homology to a human
CC sequence known per se.
SQ Sequence 339 BP: 107 A; 66 C; 65 G; 101 T;

Query Match 0.84; Score 18; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.74e+00;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 ctcttcacatctcttca 150
QY 1286 CTCTTCACATCTCTTCA 1303

RESULT 7
ID T04218 standard: DNA: 20 BP.
AC T04218:
DE Poly(ADP-ribose) polymerase beta-allele-specific DNA primer.
DE DNA primer: PCR; polymerase chain reaction; (A), sequence
KW pseudogene; Burkitt's lymphoma; B-follicular cell lymphoma;
KW small cell lung carcinoma; colorectal carcinoma; tumor;
KW breast carcinoma; ss.
OS Synthetic.

PN US5449605-A.
PR 12-SEP-1995.
PP 14-OCT-1988; 257686.
PR 14-OCT-1988; 257686.
PR 14-OCT-1988; 257686.
PA (GDF) DMV GEORGETOWN.
PI Cherney B, Lyn D, Smuleon ME;
DR wp1: 95-327692/42.
DE Allele-specific primers for detecting pre-disposition to cancer -
PT alpha-allele-specific primers for detecting pre-disposition to cancer -
CC (ADP-ribose) polymerase chromosome 13 pseudo-gene for poly
CC Claim 1: Page 31; 47pp; English.
CC This poly(ADP-ribose) polymerase beta-allele-specific DNA primer is
CC used in a method for detecting the predisposition to cancer between
CC alpha and beta alleles of the human G-protein linked receptor. This DNA
CC primer and the alpha-allele-specific primer (T04217) are based on
CC the sequence of the pseudogene (T04219-20) which flanks a region
CC which differs in size between the 2 alleles. The primers are used
CC in a PCR reaction to amplify the DNA. The resulting PCR products
CC a predisposition to cancer. A 200 bp deletion in the pseudogene on
CC chromosome-13 by amplification of regions flanking the
CC polymorphism. The primer cannot amplify chromosome-1 or -14
CC sequences. The presence of sequences of less than 200 bp indicate
CC the presence of the pseudogene.
SQ Sequence 20 BP: 2 A; 7 C; 2 G; 9 T;

Query Match 0.84; Score 17; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.74e+00;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 tcttgctctctctccg 19
Cp 1771 TCTTGCTCTCTCTCCG 1705

RESULT 8 standard: DNA: 28 BP.
AC T59623:
AD T59623:
DT 31-MAR-1997 (first entry)
DE Human G-protein parathyroid hormone receptor HRTD74 3' PCR primer.
DE G-protein parathyroid hormone receptor; HRTD74; parathormone; PTH.
KW hypophosphatemia; hypocalcemia; hypoparathyroidism; hypocalcemia;
KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphatemia;
KW kidney stone; nephrolithiasis; gene therapy; diagnosis; primer; PCR;
KW polymerase chain reaction; ss.
PN W09619433-A1.
PR 12-DEC-1996.
PP 05-JUN-1995; 007085.
PP 05-JUN-1995; 007085.
PP 05-JUN-1995; 007085.

PA (HUMA-) HUMAN GENOME SCI INC.
PI Li Y., Rosen CA, Ruben SM, Soppet DR;
DR wp1: 97-043068/04.
DE Human G-protein parathyroid hormone receptor; HRTD74 - used to
PT identify protein parathyroid hormone receptor; HRTD74 - used to
PT hypercalcaemia, hypo- or hyperphosphatemia, kidney stones, etc
PT Example 2: Page 37; 62pp; English.
CC A 3' PCR primer (T59623) contains complementary sequences to an
CC the human G-protein parathyroid hormone (PTH) receptor HRTD74
CC coding sequence (see also T59619). It was used with a 5' primer
CC (T59622) to amplify DNA encoding the PTH receptor. The PCR product
CC was incorporated into vector pGEM3/Arp to allow prodn. of
CC the PTH receptor protein. The PTH receptor protein was used to
CC amplify HRTD74 DNA suitable for incorporation into a baculovirus
CC expression system.
SQ Sequence 28 BP: 5 A; 7 C; 5 G; 11 T;

Query Match 0.84; Score 17; DB 29; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.74e+00;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 tcttcctctctctctc 28
Cp 1717 TCTTCCTCTCTCTCTC 1701

RESULT 9 standard: DNA: 35 BP.
ID 067851 standard: DNA: 35 BP.
AC 067851:
DT 20-MAR-1995 (first entry)
DE Poly(ADP-ribose) polymerase chain reaction: primer; amplification; MYVAC; ALVAC; recombinant;
KW murine; interleukin-2; IL-2; pM825; pmt-1; pM825; pM825; TK vector;
KW plasmid; vaccinia; H6 promoter; amplification; primer; antigenic response;
KW pathogenesis; human; interleukin; IFN; ss.
OS Synthetic.
PN W09416716-A.
PR 04-AUG-1994.
PP 04-AUG-1994; U00888.
PP 21-JAN-1993; US-007115.
PA (VIR-) VIROGENETICS CORP.
PI 19-JAN-1994; US-184009.
DR wp1: 94-263747/11 E, Tartaglia J;
DE Attenuated recombinant virus used for cancer therapy - comprises
PT DNA encoding cytokine and/or tumour associated antigen
PS Example 31: Page 171; 232pp; English.
CC The sequences given in 067851-56 are primers which were used in the

CC construction of an ALVAC-based recombinant virus containing the wild-
CC type murine p53 gene. Three PCR fragments were generated. Fragment I
CC was produced using primers M080 and M081 and plasmid pM825 as a
CC template. The 228 bp amplified fragment contains the H6 promoter and
CC primer M082 and M083 and plasmid p11-4 as a template. The 139 bp
CC amplified fragment contains the 3' end of the H6 promoter, the 5'-most
CC bases of the murine p53 gene, and 15 bp which overlap fragment I.
CC Fragment II was produced using primers M094 and M095 and plasmid
CC p11-4 as a template. The 139 bp amplified fragment contains the 3' end
CC of the p53 gene, and the 5' end overlaps fragment I. The three PCR
CC products were pooled and primed with M080 and M085. The resultant 588
CC bp fragment contains a BamHI site followed by H6 promoter p53. This was
CC ligated into the pM825 plasmid. The resulting plasmid containing H6 promoter
CC wildtype murine p53 is the ALVAC-Cp plasmid. The ALVAC-Cp plasmid
CC between this donor plasmid and ALVAC rescuing virus produced recombinant
CC virus vCP263, which contains the vaccinia H6 promoter murine p53 in the
CC CS locus. The resulting virus may be used in a composition for inducing
CC an immune or immunological response, ie. for immunisation against
CC pathogens.
SQ Sequence 35 BP: 11 A; 4 C; 5 G; 15 T;

Query Match 0.84; Score 16; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 8.74e+01;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 attattattgattct 16
QY 838 ATTATTATTGATTCT 853

RESULT 10 standard: DNA: 40 BP.
ID 08212 standard: DNA: 40 BP.
AC 08212:
DT 18-NOV-1995 (first entry)
DE Oligo 1 corresp. to third transmembrane domain of secretin family of
KW G-protein linked receptors. K2
KW Secretin family; G-protein linked receptor; transmembrane domain; ss.
OS Sus scrofa.
PN Key Key
PR Key Key
PP Key Key
PT Key Key
PS Key Key
CC Key Key

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Modified antibody and a recombinant for its prodn. * Includes L-chain in antibody being replaced by L-chain like protein contg. specified domain

DNA 3' sequence: 1, 1bp; Japanese pseudomonas aeruginosa antibody producing cell H1233 A H1233 gene library was prepared from the human genomic DNA and the Mu and Lambda genes were screened. The c-phase clone containing the antibody gene was analyzed and the base sequence of the gene was determined. The fusion production of the antibody was then increased and the antibody modified for inclusion of an L-chain-like protein. The sequence of the protein was then determined.

Query Match 0.84; Score 16; DB 8; Length 619;
Best Local Similarity 100.0%; Pref. No. 4.07e+01;
Matched 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 63 gccatcagcatccaggc 78
|||||
Cp 179 GCCATCAGCATCCAGC 164

RESULT 15
ID INL N30131 standard: DNA: 640 BP.
AC 750131-1992 (first entry)
NC Sequence of vp3 gene of PMDV type C3 (D250).
OS Vaccine: immunogen. antigen; viral protein; aa.
OS Foot and mouth disease virus.
CD Locden/MQualifiers
CG 1-640
FT /?tag= a
EP -686933.A.
PR 11-JUN-1982; 303040
PR 16-JUN-1981; US-274103.
PR 04-MAY-1982; US-374855.
FA (GTR) GENENTECH INC.
OR 11-SEP-1982; 303040
NP1 83-0565X/03
P-PEDB: P30199.
DR Polypeptide antigens of foot-and-mouth disease - obid. by
PP Recombinant DNA technology for vaccine prodn.
CC The inventors claim a polypeptide comprising at least one antigen of
CC PMDV, or a fusion polypeptide of at least two antigens from at least
CC two different PMDV strands, and encoding DNA. Pref. the fusion
CC of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 sequences of two of the above mentioned
CC comprise AA 55-177 or 1-210 of the VP3 virus. Fusion polypeptides

Tue Nov 24 08:10:57 1998

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9

CC	The present sequence encodes the terminal portion of the coding sequence
CC	and part of the 3'-untranslated region of the truncated hepatocyte
CC	growth factor (HGF) 2.2kb HGF/NK1. HGF/NK1 is a substantially pure
CC	truncated HGF variant comprising the N-terminal and first kringle domain
CC	of HGF. This protein has been shown by a fluorescence antibody method to
CC	mitogenicity in cells expressing well differentiated hepatoma ex vivo
CC	antigenes in cells expressing well differentiated hepatoma ex vivo
CC	under a subject in need of such cells. HGF/NK2, which is a truncated form
CC	of HGF comprising the N-terminal and the first two kringle domains, is
CC	used to inhibit HGF-induced mitogenesis in cells expressing the HGF
CC	receptor. The present sequence also encompasses the C-terminal portion
CC	of HGF/NK2. HGF/NK2 are non-toxic and bind specifically to HGFr and may
CC	therefore be used as carriers for other compounds, e.g. permitting
CC	the evaluation of the usefulness of certain toxins as chemotherapeutic
CC	agents.
Seq	Sequence 658 BP: 216 A; 126 C; 126 G; 180 T;
QW	Query Match 0.94; Score 16; DB J2; Length 658;
Bst	Best Local Similarity 100.0%; Pred. No. 4,074-01; Mismatches 0; Gaps 0;
Match	Length 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	353 cctgaagaggattgata 368
	cctgaagaggattgata 368
Cp	1305 CCTGAAGAGGATTGATA 1290
RESULT	17
AC	NC0149 standard; RNA: 693 BP.
AC	N30149:
CC	28-JUN-1992 (first entry)
CC	BLAST/PSY5 according the antigenic VP3 protein from FMDV C3 Reinde
CC	er Virus (GenBank accession number AF009492). Antigen: VP3 (FMDV C3).
CC	Vaccine; Immunogen: antigen: viral protein: na
CC	Poot and mouth disease virus.
CC	Key word Location/Qualifiers
CC	cds
CC	gene
CC	/taga a
PF	ZF--68693.1.A.
PF	05-JAN-1993 303040.
PF	16-JUN-1991 US-74103
PF	04-MAY-1992 US-374855.
PA	(CETH) GENEMATCH INC:
PA	NP1 : 83-050558/03:
DR	P-P008: P10210
DR	Polypeptide antigens of foot-and-mouth disease - obdt. by
PT	polyclonal antiserum chemistry for vaccine production.
PT	Example: Pgms 49, 81, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101,
CC	The inventors claim a polypeptide comprising at least one antigen of
CC	FMDV, or a fusion polypeptide of at least two antigens from at least

CC	two different FMDV strands, and encoding DNA. Pref. the fusion of the two strands of the genome. C. Asia 1, SAT 1, SAT 2 and SAT 3 type strains of the virus. The genome may comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. BPRI, C. Asia 1, BPRI, BPRI1, BPRI2, BPRI3, BPRI4, BPRI5, BPRI6, BPRI7, BPRI8, BPRI9, BPRI10, BPRI11, BPRI12, BPRI13, BPRI14, BPRI15, BPRI16, BPRI17, BPRI18, BPRI19, BPRI20, BPRI21, BPRI22, BPRI23, BPRI24, BPRI25, BPRI26, BPRI27, BPRI28, BPRI29, BPRI30, BPRI31, BPRI32, BPRI33, BPRI34, BPRI35, BPRI36, BPRI37, BPRI38, BPRI39, BPRI40, BPRI41, BPRI42, BPRI43, BPRI44, BPRI45, BPRI46, BPRI47, BPRI48, BPRI49, BPRI50, BPRI51, BPRI52, BPRI53, BPRI54, BPRI55, BPRI56, BPRI57, BPRI58, BPRI59, BPRI60, BPRI61, BPRI62, BPRI63, BPRI64, BPRI65, BPRI66, BPRI67, BPRI68, BPRI69, BPRI70, BPRI71, BPRI72, BPRI73, BPRI74, BPRI75, BPRI76, BPRI77, BPRI78, BPRI79, BPRI80, BPRI81, BPRI82, BPRI83, BPRI84, BPRI85, BPRI86, BPRI87, BPRI88, BPRI89, BPRI90, BPRI91, BPRI92, BPRI93, BPRI94, BPRI95, BPRI96, BPRI97, BPRI98, BPRI99, BPRI100, BPRI101, BPRI102, BPRI103, BPRI104, BPRI105, BPRI106, BPRI107, BPRI108, BPRI109, BPRI110, BPRI111, BPRI112, BPRI113, BPRI114, BPRI115, BPRI116, BPRI117, BPRI118, BPRI119, BPRI120, BPRI121, 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BPRI677, BPRI678, BPRI679, BP
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Q78979; standard: DNA; 819 BP.
 04-AUG-1995 (first entry)
 human immunoglobulin variable heavy chain #41.
 HLA-DQA1 gene, chromosome 6, polymorphic, variable; heavy chain;
 comid; placenta; vector: pVR81. P.Goli, mammalian, ds.
 Homo sapiens.

Key	Location/Qualifiers
Cds	189..639
Ft	/tag= a
Ft	/product= human immunoglobulin variable heavy chain
Ft	intron
Ft	235..337
Ft	/tag= b
Ft	/misc_signal
Ft	/tag= c
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	604..606
Ft	/tag= d
Ft	/tag= e
Ft	/tag= f
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= g
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= h
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= i
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Ft	misc_signal
Ft	640..642
Ft	/tag= j
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Ft	misc_signal
Ft	640..642
Ft	/tag= k
Ft	/note= "non-functional terminator codon"
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Ft	/tag= aa
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Ft	/note= "non-functional terminator codon"
Ft	misc_signal
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Ft	/tag= ac
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Ft	/tag= ah
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
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Ft	/note= "non-functional terminator codon"
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Ft	640..642
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Ft	misc_signal
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Ft	misc_signal
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Ft	/tag= an
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
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Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= ap
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
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Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= ar
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
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Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= at
Ft	/note= "non-functional terminator codon"
Ft	misc_signal
Ft	640..642
Ft	/tag= au
Ft	/note= "non

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PR 04-MAY-1993: US-057222.
PR (DOWC) DOWELANCO.
PR
P1 Alward LJ, Halvin KJ, Merlo DJ, Orr GL, Petell JK;
PR Proteinase 30007/US.
PR
PT -P1 by treatment with PNA lectin, amaranthin lectin or Con A lectin
P5 Disclosure: Fig. 5A-5B: 46pp. English.
CC The amino acid sequence (given in HQ8087) for the subunit which
CC contains the active site of the proteinase 30007/US is indicated
CC using preferred main codon usage to give the sequence shown in Table
CC Q76262. The synthetic sequence used to express the PNA subunit is
CC as given in Q76263. PNA encoding sequences can be used to prepare
CC recombinant lectins for use as a natural insecticide, or expressed
CC in transgenic plants for use as a natural insecticide. 253 T;
SQ Sequence 1030 BP: 276 A; 246 C; 246 G; 252 G; 253 T;
Query Match 0.84; Score 16; DB 13;
Match 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 873 ccacacatgccttc 888
CP 1756 CACACAGGCGCTC 1741
RESULT 24
AD 30007/US standard; DNM: 1200 BP.
AD HQ8087;
DE 25-JAN-1990 (first entry)
DE Glutamine synthase gene.
DE Glutamine synthetase; Inhibitors;
KW Glutamine synthetase; Inhibitors;
KW Steptomyces hygroscopicus SP-1393.
FH Key Location/Qualifiers
FH cds 134..1146
FH tag a
PR EP-333033-A.
PR 20-SEP-1989.
PR
PF 09-MAR-1989; 20189
PF 09-MAR-1989; 20189
PR (NEU) 86491; 26-10-1986
PR Kumada Y, Takano E, Nagakura K, Baba J;
PR WPI: 89-27182/38.
PR
DR C-PDS; P31288.
DR Glutamine synthetase gene encoding glutamine synthetase - resistant to
DR glutamine synthetase inhibitors, used to produce plants resistant to
PR blalaphos and L phosphinothricin.
PR Clain 2; fig. 4; 14pp. English.
CC The coding sequence of a new glutamine synthetase gene (GLN-BP) and tag a represents
CC is resistant to glutamine synthetase inhibitors e.g. the herbicides

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SQ      and 9.6.          Sequence 1260 BP:   457 A:   167 G:   219 G:   417 T:
Query Match            0.84; Score 16; DB 22; Length 1360;
                        Similarity: 16; And 4.00;
Match 16; Conservative    0; Mismatches 0; Indels 0; Gaps 0;

Db      1080 atggaatttttggcct 1095
Cp      757 ATGGGATTTTGGCGGT 742

RESULTS 26
AC      G11381 standard; DNA: 1287 BP.
AD      G11381.
DE      07-NOV-1991 (first entry)
DT      Human beta2-adrenergic-SR2 hybrid receptor (1).
DS      Human beta2-adrenergic-SR2 hybrid receptor; screening: internal;
EA      extracellular; N-terminal; C-terminal; effects; domain se.
FH      Key Location/Qualifiers
FT      miscRNA      1..147
FT      /cseg       nucleotides 1-147 of yeast G
FT      /protein     protein-coupled receptor.
FT      /cseg       b
FT      /misc_rna    148..1287
FT      /cseg       b
FT      /protein     protein-coupled receptor.
FT      /cseg       b
FT      /misc_rna    103-1242 of human G protein-
FT      /cseg       coupled receptor.
FT      /cseg       b
FT      /misc_rna    WO9112273-A.
PD      22 AUG-1991.
PN      000909
PP      08 FEB-1990. US 478100.
PA      (ZMVC) ZYMOTGENETICS INC.
PA      Sledzickak AZ, Sheppard PO:
PR      Protein J. 25100/36.
PI      25100/36.
PT      Producing hybrid G-protein coupled receptors - mammalian DNA
PT      sequenced encoding receptors having at least one domain replaced
PT      by corresp. Yeast domain used to transform yeast host cells
PT      by corresp. Yeast domain used to transform yeast host cells
CC      The hybrid beta2-ADR-SR2 receptor was constructed by replacing the DNA
CC      sequence encoding the extracellular N-terminal domain of a DNA
CC      sequence encoding the intracellular N-terminal domain of the
CC      construct with the corresponding gene product.
CC      Constructed plasmids were transformed together with a TP11
CC      transcriptional promoter and terminator. The construct is used to
CC      transform yeast cells. For the detection of the presence of a ligand in
CC      a test sample, the culture of the yeast cells may be exposed to the test
CC      substance. The response of the yeast cells to the substance is measured.
CC      Response to the ligands can be easily monitored. The method is useful
CC      screening for potential G protein-coupled receptor ligands is less

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CC bacillophos and L-phenylalanine. The gene may be used to produce plants
SQ Sequence 1200 BP; 196 A; 428 C; 416 G; 160 T;
Query Match      0.8%   Score 16; DB 1; Length 1200;
Best Local Similarity 100.0%; Prod No. 4.0e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 341 cctgctgtgcggcg 356
Cp 1471 CTCTGTGCGTGGCG 1456

RESULT 25
ID TL7043 standard; DNA; 1260 BP.
AC AT17043;
DT 04-OCT-1986 (first entry)
DE B.thuringiensis insecticidal protein gene jg890 (partial sequence).
KW Bacillus thuringiensis ser. jegathesan 367;
KW Aedes aegypti; Anopheles stephensi; Culex pipiens; Stig 367; ss.
KW Bacillus thuringiensis ser. jegathesan 367.
FH Key Location/Qualifiers
FT 1..1260
FT /product= partial_Jeg890_protein
FT /note='partial CDS only; stop codon is not
FT included'
FT /tag=b
FT misc_feature
FT /note='corresponds to amino acid sequence
FT determined by direct microsequencing'.
W09606371-A2
PD 29-FEB-1992
PR 24-AUG-1995; F0116.
PR 25-AUG-1994; FR-010299.
PA DLSNP, INST PATENT.
PA WPI: 96-151374/15
DR WI: 96-151374/15
DR P-PDB: R33080.
DR New B.thuringiensis ser. jegathesan insecticidal proteins - and
DR je890, je891, je892, je893, je894, je895 isolated from
DR Bacillus thuringiensis ser. jegathesan against dipteran larvae, e.g.
DR A. aegypti, A. stephensi or C. pipiens.
GC Claim 3; Page 33; 55pp; French.
CC The present invention is a partial coding region and 5'-non-coding
CC region of the genes encoding the Jg890 gene, 307 (nt), isolated from
CC Bacillus thuringiensis ser. jegathesan, which encodes a crystal
CC encodes a crystal toxin which is active against dipteran insects,
CC esp. mosquitoes. The full-length, recombinant Jg890 toxin, had mean
CC LC50 values (in ng/ml) after 48 hours of 18.6, 42.7, and 10.1 against
CC A. aegypti, A. stephensi and C. pipiens, respectively. Wild-type
CC respectively. Wild-type Stig367 crystals gave values of 2.7, 54.5

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CC expensive and labour intensive than previous methods and does not
CC necessitate the isolation of membrane fragments from responsive
CC tissues or cell lines.
CC Other exemplary DNA sequences encoding hybrid C protein-coupled
CC receptors are as follows: (1) the C-terminal internal effector
CC domain of the *Escherichia coli* histidine kinase, (2) the C-terminal
CC internal effector domain are replaced, and (3) the N-terminal
CC extracellular domain, the third internal effector domain and C-
CC terminal internal effector domain are replaced; all with the
CC sequence of the S. cerevisiae STE2 gene.
CC See also 013493-83.
SQ Sequence 1287 BP; 294 A; 333 C; 314 G; 346 T;
Query Match: 0.89; Score 16; DB 2; length 1287;
Maximal Similarity 100.0%; Start 40; End 40;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 385 gctctgctgcctcgg 400
Cp 1465 GTCTGTCGCTGACGG 1450
RESULT 27
ID: 065353 standard; DNA; 1340 BP.
AC AC053533;
DT 06-NOV-1994 (first entry)
DE Outer membrane lipoprotein A gene from clone HB101/pOH37/E15.
OS *Escherichia coli* O157:H7
KE Acetobacillus pleuropneumoniae
FY 060100
FX Genbank
FH Key
FI Location/Qualifiers
FT 137..1204
FT cds
FT /tag= a
FN W09410316-A.
PD 11-MAY-1994.
PF 03-NOV-1993; CA0448
PF 03-NOV-1993; CA0458
PR 03-NOV-1993; CA0468
PT (UTR)+ UNIV SRA24CTHEWAN
PT (UTR)+ UNIV SRA24CTHEWAN
PI Gettick GF, Porter AA, Rossi-campoa A, Willson PJ;
DR WP: 94-157471/20.
DR P-258B; R54666; *Acetobacillus pleuropneumoniae* outer membrane lipoprotein -
DR used in vaccines for treating or preventing infection, partic. in
PT pigs and for diagnosis
PF Clinia J; pig 1: 5pp; English.
PE Protein (contig) was isolated and analyzed. AP culture supernatant
CC protein (contig) was isolated and analyzed. AP culture supernatant
CC was used to raise rabbit antiserum which was used to screen an AP
CC strain AP 37 genomic DNA library in λ coat to obtain DNA encoding
CC an APTotype. Cloning the protein prod. of the gene can be used in
CC the same way as the APTotype. The protein prod. of the gene can be
CC used as a probe for detecting AP and for detecting homologous genes

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UU-068-011A-1.rn

CC in other bacterial strains.
CC See also Q6534.
SQ Sequence 1340 BP; 500 A; 185 G; 262 C; 393 T;
      0.8%; Score 16; DB 10; Length 1340;
      Query Match: 100.0%; Pred. No. 4.07e-01;
      Best Local Similarity 100.0%;
      Matches 16; Conservative 0; Mismatches 0; Indels 0;

Db 350 gaaccacaaagatgcg 365
Cp 562 GAACCAAAAGATGC 547

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RESULT      28
ID          GS4397 standard; DNA, 1150 BP.
DT          06-JUL-1994 (first entry)
DE          Peline Immunodeficiency Virus (No isolate) gag gene.
EM          FIV; French virus strain; No isolate; glycoprotein;
KW          feline acquired immunodeficiency syndrome; cat; vaccine;
KW          retrovirus; lentivirus; ss.
KW          Antic ImmunoDeficiency Location/Qualifiers.
FR          FR-014026
FT          cd5
FT          1..1150
FT          /tag= a
FT          /product= Gag reading frame does not include
FT          initiation or termination codons".
PN          EP-57748-A.
PD          05-JAN-1994. 401338.
PF          16-JUN-1993. 401338.
PR          16-JUN-1993. FR-007258.
PR          16-JUN-1993. FR-007258.
PR          23-NOV-1992. FR-014026.
PA          (CNRS ) CNRS CENT NAT RECH SCI.
PI          Avramas A., Chappey C., Kiatmann D, Morallion A.
PI          Pincino G., Saurin W, Sonigo P, Strobsbery AD.
PI          P-509B. 844958.
DR          P-509B. 844958.
PT          Nucleic acid sequences of Gag and Env genes - of feline immune
PT          deficiency virus, strain No, and derived probes, primers, vectors
PT          and peptide(s). For diagnosis and vaccination
PS          Claim 3, Page 31-33: Soggs; French
CC          infected with the FIV French strain No were co-cultured with PL-2
CC          from uninfected cats in the presence of recombinant human IL-2
CC          concanavalin A. After 15 days, total cellular DNA was extracted
CC          from cells positive for Mg-dependent reverse transcriptase acti
CC          genes. PCR primers were designed based on conserved regions of
CC          Petaluma isolate of FIV. The gag gene was obtained from 2

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CC   overlapping subfragments.
80   Sequence      1150 BP: 481 A; 232 C; 329 G; 308 T;
      Query Match 0.88; Score 17; DN % 9; Length 1350;
      Query Match similarity 100.0%; 828 A; 2400 G;
      Matches 17: Conservative G; Mismatches 0; Indels 0; Gaps 0;
DB   db 1113 aggtacgaccaccatg 1129
CP   cp 1198 AGGACGACGACAGTGT 1182

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RESULT      29
ID          ID T30647 standard: DNA; 1368 BP.
AC          AC T30647
DE          DE Hspg3_1896 (first entry)
PR          PR P. gingivalis haemagglutinin gene hspg3
KW          KW Haemagglutinin; hspg gene; periodontal disease; vaccine; probe;
            KM Hspg3; as.
OR          OR Porphyromonas gingivalis strain 301.
DR          DR J94060
IN          IN EMBL
PD          PD 11-DEC-1995; U16108.
PP          PP 09-DEC-1994; US-35485.
PT          PT (UNR.) UNR RES FOUNDED.
PA          PA (H.T.) FLORIDA.
AU          AU M. Lantz Jr., Leptine G, Patti JM, Regulante-Fox A;
            PI Tuwanoon S;
            WP1. 96-287181/29.
P-PEDIR     P-PEDIR: RS6023.
ORPHONAMES  ORPHONAMES: gingivalis genes and proteins - used in the detection
            OF: Porphyromonas gingivalis periodontal disease
            CLAM 6 Claim 6: Page 108-110; 15pp; English.
            HSPG3 (T30647) as the third repeat unit in a repeat region of the
            hspg gene (T30654) of P. gingivalis 318. It encodes a portion
            (residues 1-30) of the 281-kDa haemagglutinin hspgA (J96010) of P.
            CC CCC 30654). The hspgA gene can be used for the production of recombinant antigens useful in
            CC CCC vaccines against periodontal disease. They can also be used as
            CC CCC probes to detect evidence of periodontal disease.
            SQ Sequence 1368 BP; 348 A.; 339 C.; 351 G.; 330 T.
            Query Match 0.8%; Score 16; DB 21; Length 1368;
            Best Local Similarity 100.0%; Pred. No. 4.07e+01;
            Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB          DB 1039 objects; query sent 1048
OY          OY 381 GTTCCTTCGCAGACT 396

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US-08-068-011A-1.mzn

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RESULT: 30
AC 128972 standard; cDNA; 1374 BP.
AD 128972
DT 31-AUG-1996 (first entry)
DE Mouse CRF receptor genomic clone mCRF-RM1
KW CRF receptor; CRF; CRF factor receptor; CRF-R; corticoliberin
KW KW translation; 48

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OS Mus sp.                               Location/Qualifiers
FH Key                                     /79..1374
FI cds                                    ?/cdgs+ a
PI W06617834.A-2
PD 13-JUN-1996.
PF 06-DEC-1995. U15909.
PR 09-DEC-1994: US-353537.
PR 12-JAN-1995: US-3740097.
PT 16-MAR-1995: S. BIOLOGICAL STUDIES.
PI Chen R., Donaldson C.J., Lewis RA., Perrin MH., Savchenko P.;
PI Vale WW;
PI WP1: 96-287179.9.
DR P-F50B: R97293.
DR P-F50B: R97293.
PT Located corticotropin-releasing factor receptor (CRF-R) - used to
PT designed primers for amplifying digital transduction activity mediated
PT by CRF-R.
CC Claim 6: Page 83: 102pp: English.
CC A genomic clone (728972) codes for mouse corticotropin
CC releasing factor receptor mCRF-RH1 (R97293). It was isolated
CC from a rat brain cDNA library (R97293) by PCR amplification
CC by PCR amplification (see also T24973-74) of an exon of mCRF-RB1
CC The mCRF-RB1 cDNA can be used as a probe for detecting the presence
CC of CRF receptor-encoding nucleic acids in samples or for the
CC identification of additional CRF receptors, or can be used for producn.
CC specific antisense type II receptor, or in gene therapy to target a vector to
CC specific cell types.
SQ Sequence 1374 BP: 279 A; 421 G; 344 G; 330 T;
Query Match 0.84; Score 17: DB 20; Length 1374;
Best Local Similarity 100.0%; Prod. No. 874ter00;
Matches 17; Conservative 0; Mismatches 0; Gaps 0;
Db 1189 caggggtttcttctgc 1205
| | | | | | | | | | | | | | | |
OY 1302 CAGGGGTTCCTTCTGC 1318
RESULT 31
ID ID Q38027 standard: cdNA: 1393 BP.
AC AC Q38027:
DB 16-JUN-1993
CD CD
KW TOBACCOS: GUANAYE ALSOHOP dehydrogenase; QAD: tryptic peptide: primer:

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Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 38
 ID T10057 standard: cDNA: 1603 BP.
 AC T70057;
 DT 20-AUG-1997 (first entry)
 DE Cotton fibre specific cDNA clone H4.
 KW Cotton fibre promoter; transgenic plant; truncated;
 OS Gossypium barbadense strain Sea Island.
 PN US5620982-A.
 PP 04-OCT-1988: 253243.
 PR 04-OCT-1988: US-253243.
 PR 21-NOV-1990: US-617239.
 PR 18-MAY-1992: US-895970.
 PA (CETU) AGRACETUS INC.
 PI John N;
 DR WPI; 97-235195/21.
 PT Altered fibre-specific promoters - used for introducing
 PT Cotton fibre specific cDNA clones (T10057) into plants.
 PS Example 3; column 49-50; 48pp; English.
 CC T70040-57 are cotton fibre-specific cDNA clones which can be used to
 CC obtain genomic clones containing fibre-specific promoters. Claimed DNA
 CC clones have been used to produce transgenic plants from cotton cells.
 CC that promote preferential gene expression in plant fibre cells.
 CC protein coding sequence not naturally associated with the promoter
 CC sequence and a 3' termination sequence. The DNA constructs are useful for
 CC expressing foreign genes in fibre-producing plants, esp. to produce
 CC cotton fibre with enhanced quality. The present sequence comprises H4 cDNA isolated from clone
 CC SIFB10-H4 (SI = Sea Island; FB10 = 10 day old bolls).
 CC Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;
 QY Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.07e+01; Length 1603;
 Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 39
 ID T10267 standard: DNA: 1603 BP.

Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 38
 ID T10057 standard: cDNA: 1603 BP.
 AC T70057;
 DT 20-AUG-1997 (first entry)
 DE Cotton fibre specific cDNA clone H4.
 KW Cotton fibre promoter; transgenic plant; truncated;
 OS Gossypium barbadense strain Sea Island.
 PN US5620982-A.
 PP 04-OCT-1988: 253243.
 PR 04-OCT-1988: US-253243.
 PR 21-NOV-1990: US-617239.
 PR 18-MAY-1992: US-895970.
 PA (CETU) AGRACETUS INC.
 PI John N;
 DR WPI; 97-235195/21.
 PT Altered fibre-specific promoters - used for introducing
 PT Cotton fibre specific cDNA clones (T10057) into plants.
 PS Example 3; column 49-50; 48pp; English.
 CC T70040-57 are cotton fibre-specific cDNA clones which can be used to
 CC obtain genomic clones containing fibre-specific promoters. Claimed DNA
 CC clones have been used to produce transgenic plants from cotton cells.
 CC that promote preferential gene expression in plant fibre cells.
 CC protein coding sequence not naturally associated with the promoter
 CC sequence and a 3' termination sequence. The DNA constructs are useful for
 CC expressing foreign genes in fibre-producing plants, esp. to produce
 CC cotton fibre with enhanced quality. The present sequence comprises H4 cDNA isolated from clone
 CC SIFB10-H4 (SI = Sea Island; FB10 = 10 day old bolls).
 CC Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;
 QY Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.07e+01; Length 1603;
 Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 39
 ID T10267 standard: DNA: 1603 BP.

Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 37
 ID T10305 standard: cDNA: 1603 BP.
 AC T13050;
 DT 16-DEC-1996 (first entry)
 DE Cotton fibre promoter; transgenic plant; crop improvement; da.
 KW Cotton fibre promoter; transgenic plant; crop improvement; da.
 OS Gossypium barbadense strain Sea Island.
 PN US495070-A.
 PP 04-OCT-1988: 253243.
 PR 04-OCT-1988: US-253243.
 PR 21-NOV-1990: US-617239.
 PR 18-MAY-1992: US-895970.
 PA (CETU) AGRACETUS INC.
 PI John N;
 DR WPI; 96-139095/14.
 PT New isolated fibre-specific promoters - used for introducing
 PT Altered fibre-specific characteristics into plants, partic. cotton.
 CC Cotton cDNA clone H4 (T10305) was isolated from a cDNA library of
 CC cotton var. Sea Island using a subtractive hybridization procedure.
 CC The clone hybridises to fibre RNA, and to a much lesser extent to
 CC petal RNA and other fibre-specific cDNA clones (see T10033-49).
 CC Isolation of genomic clones (see T10033-12 and T10032-53) contg.
 CC sequences capable of promoting gene expression in fibre cells.
 CC Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;
 QY Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.07e+01; Length 1603;
 Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 38
 ID T10057 standard: cDNA: 1603 BP.
 AC T70057;
 DT 20-AUG-1997 (first entry)
 DE Cotton fibre specific cDNA clone H4.
 KW Cotton fibre promoter; transgenic plant; truncated;
 OS Gossypium barbadense strain Sea Island.
 PN US5620982-A.
 PP 04-OCT-1988: 253243.
 PR 04-OCT-1988: US-253243.
 PR 21-NOV-1990: US-617239.
 PR 18-MAY-1992: US-895970.
 PA (CETU) AGRACETUS INC.
 PI John N;
 DR WPI; 97-235195/21.
 PT Altered fibre-specific promoters - used for introducing
 PT Cotton fibre specific cDNA clones (T10057) into plants.
 PS Example 3; column 49-50; 48pp; English.
 CC T70040-57 are cotton fibre-specific cDNA clones which can be used to
 CC obtain genomic clones containing fibre-specific promoters. Claimed DNA
 CC clones have been used to produce transgenic plants from cotton cells.
 CC that promote preferential gene expression in plant fibre cells.
 CC protein coding sequence not naturally associated with the promoter
 CC sequence and a 3' termination sequence. The DNA constructs are useful for
 CC expressing foreign genes in fibre-producing plants, esp. to produce
 CC cotton fibre with enhanced quality. The present sequence comprises H4 cDNA isolated from clone
 CC SIFB10-H4 (SI = Sea Island; FB10 = 10 day old bolls).
 CC Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;
 QY Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.07e+01; Length 1603;
 Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 39
 ID T10267 standard: DNA: 1603 BP.

Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 37
 ID T10305 standard: cDNA: 1603 BP.
 AC T13050;
 DT 16-DEC-1996 (first entry)
 DE Cotton fibre promoter; transgenic plant; crop improvement; da.
 KW Cotton fibre promoter; transgenic plant; crop improvement; da.
 OS Gossypium barbadense strain Sea Island.
 PN US495070-A.
 PP 04-OCT-1988: 253243.
 PR 04-OCT-1988: US-253243.
 PR 21-NOV-1990: US-617239.
 PR 18-MAY-1992: US-895970.
 PA (CETU) AGRACETUS INC.
 PI John N;
 DR WPI; 96-139095/14.
 PT New isolated fibre-specific promoters - used for introducing
 PT Altered fibre-specific characteristics into plants, partic. cotton.
 CC Cotton cDNA clone H4 (T10305) was isolated from a cDNA library of
 CC cotton var. Sea Island using a subtractive hybridization procedure.
 CC The clone hybridises to fibre RNA, and to a much lesser extent to
 CC petal RNA and other fibre-specific cDNA clones (see T10033-49).
 CC Isolation of genomic clones (see T10033-12 and T10032-53) contg.
 CC sequences capable of promoting gene expression in fibre cells.
 CC Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;
 QY Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.07e+01; Length 1603;
 Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 38
 ID T10057 standard: cDNA: 1603 BP.
 AC T70057;
 DT 20-AUG-1997 (first entry)
 DE Cotton fibre specific cDNA clone H4.
 KW Cotton fibre promoter; transgenic plant; truncated;
 OS Gossypium barbadense strain Sea Island.
 PN US5620982-A.
 PP 04-OCT-1988: 253243.
 PR 04-OCT-1988: US-253243.
 PR 21-NOV-1990: US-617239.
 PR 18-MAY-1992: US-895970.
 PA (CETU) AGRACETUS INC.
 PI John N;
 DR WPI; 97-235195/21.
 PT Altered fibre-specific promoters - used for introducing
 PT Cotton fibre specific cDNA clones (T10057) into plants.
 PS Example 3; column 49-50; 48pp; English.
 CC T70040-57 are cotton fibre-specific cDNA clones which can be used to
 CC obtain genomic clones containing fibre-specific promoters. Claimed DNA
 CC clones have been used to produce transgenic plants from cotton cells.
 CC that promote preferential gene expression in plant fibre cells.
 CC protein coding sequence not naturally associated with the promoter
 CC sequence and a 3' termination sequence. The DNA constructs are useful for
 CC expressing foreign genes in fibre-producing plants, esp. to produce
 CC cotton fibre with enhanced quality. The present sequence comprises H4 cDNA isolated from clone
 CC SIFB10-H4 (SI = Sea Island; FB10 = 10 day old bolls).
 CC Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;
 QY Sequence 1603 BP; 385 A; 345 C; 393 G; 480 T;

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.07e+01; Length 1603;
 Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 tctgtggaacttagtg 174
 QY 1005 TCTGTGGAACCTAGTG 1020

RESULT 39
 ID T10267 standard: DNA: 1603 BP.

	RESULT	41	ID Tl1314 standard; DNA: 1689 BP.	
AC	CT	Tl1314:	(first entry)	
CC	DD	23-NOV-1996	G genomic DNA,	
CN	EE	CG-chromokine receptor 3 CRK-3;	Eos-L2; inhibitor: antisense;	
KW	FH	cGMP-Kinase; eoslnophilic; db.		
OS	FR	X-ray	Location/Qualifiers	
PB	GG	Homo sapiens	/taxid= "9607"	
PF	HH	CD4	/tag= "a"	
PT	IJ	variation	/tag= "1007..1008"	
FF	JL		/tag= "b"	
FT	KL		/tag= "c"	
FF	LJ		/tag= "d"	
FF	MJ		/tag= "e"	
FF	NJ	misc_difference 1391	"base n at position 1291 is not identified in the specification".	
FF	OJ			
FP	PK	W09622371-A2.		
PD	PL	25-JUL-1996	UO60608	
PR	PM	18-MAY-1995	US-1375199	
PPA	PN	18-JAN-1995	US-1375199	
PA	PO	(BCIM) BRIGHAM & WOMENS HOSPITAL.		
PPA	QO	(CHIL-) CHILDRENS MEDICAL CENT.		
PA	RJ	(LEUK-) LEUCODIAG INC.		
PPA	SJ	Bethesda G.C., Gerard NP., Mackay CR., Penath PD., Post TM; OI = 95-354528/35. MPI : 96-334528/35.		
DR	SD	P-PDBD: W03376.		
DF	TD	Mammalian chemokine receptor-3 and related nucleic acids - useful to diagnose and treat autoimmune disorders, certain cancers, etc.		
PT	UD	Claim 1: Page 109; US3pp: English.		
PS	VE	A generic DNA clone (Tl1314), codes for a novel receptor (W03376), designated Eos L2 or C-C chemokine receptor 3 (CRK-3). Involved with allergic rhinitis and asthma.		
CCC	VF	The gene was isolated from a human genomic library in EMBL3 SP7/T7 vector by screening with a PCR fragment generated from eoslnophil CDNA using degenerate primers (see also Tl1337-44).		
CCC	VF	The sequence of cDNA determined here corresponds exactly to that given in Tl1316. A value indicated cDNA consensus sequence for Eos L2 has been added.		
CCC	VG	The prodn. of recombinant CRK-3 in host cells, or to design antisense sequences useful for treating inflammatory disease.		
CCC	VH	sequence 1689 BP: 431 A; 418 C; 344 G; 497 T.		
DQ	VJ	Query Match 0.9% Score 16: DB 23: Length 1689: Best Local Similarity 100.0%; Ref. No. 4,07e+01:		

Query Match 0.88; Score 16; DB 23; Length 1689;
Best Local Similarity 100.00; Pred. No. 4.07e+01;

[illegible]

Query Match 0.8%; Score 16; DB 32; Length 1689;
Best Local Similarity 100.0%; Pred. No. 4.07e+01;

```

Cp 1337 CCGATGACGACGACGATG 1322

RESULTS 43
AD Q13573; standard; DNA; 1810 BP.
AC Q13573;
DT 29-NOV-1991 (first entry)
DE E75B specific exon 81.
DS Transcription unit; Inset steroid receptor; hormone: es.
SW Drosophila melanogaster.
SK Key Words: Location/Qualifiers
FH Key 249..1800
FT mRNA
FT cda 51597..a
FT cda 51597..a
FT /tag= a
FT /tag= a
FT intron 1801..1810
FT /tag= c
FT /note= 1st 10 nucleotides of intron E75B.
W05113167.A.
05-SEP-1991.
15-FEB-1991; D01189
15-FEB-1991; D01189
PA (STED) LELAND STANFORD JR UNIV.
PI Hogness DS, Koelle MR, Segraves WA;
WP1: 91-281480/38.
DR PUBMED: 813792.
DR PUBMED: 813792.
PT Drosophila melanogaster steroid receptors - and ligands, for use as
PT benign inducing factors.
PT Claim 2: Page 100; 126pp; English.
PS The DNA sequence encodes the E75B specific exon 81 which is located
PS within the 5' noncoding region of the E75B gene. The description
PS unit. The intron shown links the 81 to exon 2. The two
PS transsplicing units together make up the E75 gene. It displays
PS characteristic Drosophila melanogaster codon usage. The E75
PS receptor family encodes the putative hormone binding E domain of
PS E75 proteins does not show high sequence homology to the known
PS ecdysone receptor (Q13574) it is likely that the E75 proteins bind
PS a novel hormone or a novel Drosophila hormone.
PS See also Q13572-Q13575.
SQ Sequence 1810 BP; 568 A; 502 C; 475 G; 265 T;
Query Match 0.84; Score 16; DB 2; Length 1810;
Query Local Similarity 100.0%; Pred. No. 4,07+01;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 1057 caccacacacacacacacacac 1072
QY 1460 CAGCAGCAGCAGCAGCAGC 1475

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Query Match      0.8%  Score 16; DB 2; Length 1810;
Best Local Similarity 100.0%  Pred. No. 4.07e+01;
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DB	1037	cagcaccagcagccag	1072
QY	1460	cagcaccagcagccag	1475

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RESULT . 44
ID T15945 standard; cDNA. 1862 BP.
AC T15945-1986 (flag entry)
AD Opusum Kidney PTHrP/PTHrP receptor cDNA clone OK-H.
KW Parathyroid hormone-related protein; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer; opusum; transgenic animal;
OS Delphida virginiana.
DE Key Location/Qualifiers
FT 98..1645 /tag= a
FT cda
PN US5494806-A.
PP 27-FEB-1996.
PP 05-APR-1991; 681702
PP 06-APR-1991; US-864472
PP 06-APR-1991; US-864472
PI (GENO.) GEN HOSPITAL CORP.
PI Abou-Samra A., Juppner H., Kronenberg HM, Potts JT;
PI WPTSPG-13902; Syntex CV;
PI P-PDSB: R32725.
DR DNA encoding vertebrate parathyroid hormone receptor - useful for
DI diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PG Claim 1 Fig 1A-1E: 64pp; English.
CC A cDNA clone (T15945), designated OK-H ATCC 68573), codes for a
CC parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptor [J92782]. To obtain OK-H, an opusum kidney (OK) cell cDNA
CC library was screened by hybridization with a PTHrP probe. Several
CC were selected for ability to bind labelled PTH. Another cDNA clone,
CC OK-O (T15946), was also isolated in this screening. OK-H and OK-O
CC may represent 2 separate genes or may result from a laboratory
CC system. The two clones can be used for diagnostic purposes as well
CC as research. The host cells can also be used for diagnostic pur-
CC poses at the serum levels. Transgenic chickens that overexpress the element
CC of PTHrP are available.
SQ receptor in their oviduct lay eggs of higher calcium content.
SQ sequence 1862 BP; 406 A; 495 C; 521 G; 438 T;
Query Match 0.89; Score 17; DB 18; Length 1862;
Matches Local Similarity 100.0%; Pred. No. 8.74e+00;
Base 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 971 tgcattctcgtggagcg 987
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Oy 846 TGACTCTCTCGTGAGC 862
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RESULT 45
ID Q35605 standard; cDNA. 1863 BP.

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DB   971 tgcattcttggcgaagg 987
QY   846 TGCATCTCTGGTGAAGG 862

RESULT 46
ID    TI5946 standard; cDNA; 1863 bp.
CC    OT5946: 1996 (filar artery)
DD    Opacium kidney PTH/PTHrP receptor cDNA clone OK-O.
DE    Parathyroid hormone-related protein; parathormone; PTH.
KW    Parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW    hypercalcaemia; hypercalcaemia; cancer; opacium; transgenic animal;
OS    Bidelhuisia hystrix.
OS    Bidelhuisia virginiana.
FH    Key Location/Qualifiers
FT    cds 98..1855
FT    /tag= a
PI    DB5494806-A.
PD    27-FEB-1996.
PP    05-APR-1991: 631702.
PP    05-APR-1991: US-681702.
PP    05-APR-1991: US-681702.
(PZ) (GEN) GEN HOSPITAL CORP.
PA    Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI    Schipani E, Segre AV.
PI    Endocrinology 120:276-84.
PI    P-PDB: R32726.
PT    DNA encoding vertebrate parathyroid hormone receptor - useful for
PT    diagnosis and treatment of e.g. hypocalcaemia, hypo-calcaemia,
PS    Glain I; Fig 2A-2E; 64pp; English.
CC    A cDNA clone (TI5946), designated OK-O AFCC 68572), codes for a
CC    parathyroid hormone-related hormone-related protein (PTHrP/PTHrP).
CC    The complementary DNA was obtained from rat parathyroid kidney (OK) cDNA
CC    library in pCMVcat vector on Oncor's Cosmid Constructing Kit. This
CC    library is optimal for use in transient expression systems.
CC    We selected for ability to bind labelled PTH. Another cDNA clone,
CC    OK-H (TI5945), was also isolated in this screening. OK-H and OK-O may
CC    represent 2 separate genes or may result from a laboratory artifact.
CC    Transgenic mice expressing OK-O have been generated. These mice are
CC    suitable for studying the role of PTHrP in bone metabolism and endocrine
CC    systems. The host cells can also be used for diagnostic measurement
CC    of PTH serum levels. Transgenic chickens that overexpress the
CC    receptor in their oviduct lay eggs of higher calcium content.
CC    Query Match 1863 BP. 400 A. 495 C. 312 G. 438 Y.
Query Match 0.88; Score 17; DB 18; Length 1863;
Best Local Similarity 100.0%; Ref No. 674e+00;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB   971 tgcattcttggcgaagg 987

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US-08-468-011A-1.rnq

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Q02605:
16-MAR-1993 (first entry)
Opasum Kidney PTH/PTHrP receptor clone, OK-O.
Parathyroid hormone related protein; calcitonin;
Dialupia virginiana; calcemia; as.
Key Location/Qualifiers
FH Key Location/Qualifiers
cda 98.1855
/ tag = a
PM W09217602-A.
PD 15-OCT-1992.
PD 06-APR-1993. U02821.
PR 05-APR-1993. U02821.
PR 05-APR-1993. U02821.
PA (GENE) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV. 166971/44.
PD P-58083 R27705.
DR New DNA encoding parathyroid hormone receptor, DNA and antibodies
- for (differential) diagnosis of hypercalcaemia, and diagnosis
- treatment of two cases.
CC Total RNA was isolated from opasum kidney (OK) cells and used to
CC prepare a cDNA library. The resultant phage libraries were used to
CC transform E. coli using a larger helper plasmid p1. The cells were
CC infected and the phage libraries were screened for the presence of
CC parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor proteins, performed according to Geisler et al., (EMBO J.
CC 8: 3676, 1989), by identifying colonies capable of binding a
CC OK-His6 radiolabeled ligand. The clone OK-H is identical to the
CC OK-His6 radiolabeled ligand. The clone OK-H encodes one of five
CC alpha protein, OK-H encodes one of five amino acids. The difference
CC attributed to a single nucleotide deleted in the OK-H sequence causing
CC a frame shift and an earlier stop codon. It is not known whether OK-H
CC is a true ligand or a receptor. The clone OK-H is a cDNA library
CC artifact. The clone encodes a protein which may be used in a
CC therapeutic compas. To inhibit activation of PTH or PTHrP and thus
CC reduce the level of calcium in the blood. Cds. capable of competing
CC with PTH or PTHrP for binding to the PTH/PTHrP receptor. The
CC and DNA homologous to PTH DNA can be identified using fragments of
CC the clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC hypercalcaemia. The sequence may be used for the prodn. of antibodies
CC ligand such as in hypercalcaemia. The sequence may be used for the
CC prodn. of antibodies.
CC Sequence 1863 BP: 441 A: 494 C: 518 G: 518 T: 518
Query Match: 0.0% Score 17; Pos 5 Length 1863;
Bad Local Similarity 100.0%
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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113-08-468-011A-1. yna

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QY      846 TGGATCTGCGAGACG 852
        /
RESULT  47
AD      T89162 standard; cDNA; 1915 BP.
AC      T89162
DT      14-DEC-1987
DE      Human chemokine receptor 88-2B cDNA.
KW      Chemokine receptor 88-2B; Atherosclerosis; rheumatoid arthritis;
KW      autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW      G protein coupled receptor; human; aa.
OS      Homo sapiens.
Key     Location/Qualifiers
ID      cDNA              302..479
            /tag= a
FT      P=DSB;T2698/A2.
PT      PD 26-JUN-1997. U30759
PR      07-JUN-1986; U5-61139.
PR      20-DEC-1985; U5-575967.
FA      C100S-1 ICOS CORP.
WPI     97-341689/31.
DR      P-PSDB;T71214.
DD      New nucleic acid encoding chemokine receptors 88-2B and 88C - used
          to determine their function in monocytes trafficking. g. for treatment of
          inflammation.
CC      Clin 7; Page 48-50; 65pp; English.
CC      This sequence comprises a full-length cDNA coding for novel human
          chemokine receptors 88-2B and 88-2C. Receptor 88-2B was obtained
          from a macrophage cDNA library using 88-2B-specific primers. A
          full-length clone (see T89161) for chemokine receptor 88C (T71213)
          was also obtained. 88C and 88-2B cDNAs can be used to produce
          recombinant proteins for studies of their functions in the
          treatment of e.g. atherosclerosis, rheumatoid arthritis, tumours,
          asthma, viral infection, AIDS and inflammatory conditions. Nucleic
          acid fragments can be used to isolate genomic sequences, to detect
          polymorphisms, to generate probes for Northern blotting and to
          receptor genetics to facilitate identification of modulators and
          to produce knockout animals, and (antisense forms) to alter/study the
          genetics and expression of the receptor.
          Sequence 1915 BP. 488 A. 470 C. 373 G. 584 T.
Query Match 0.8% Score 16 DB 34 Length 1915;
Match Local Similarity 100.0% Pred. No. 4.07e+01;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db      1572 gcagatcagctagats 1587
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07-OCT-1997.
24-MAR-1997: J00982.
PR (DAIN) DAINPENTON PHARM CO LTD.
PA (DAIN) DAINPENTON PHARM CO LTD.
PP (DAIN) DAINPENTON PHARM CO LTD.
DR P-PDB; N34330.
DR P-PDB; N34330.
Novel beta-2 adrenergic receptor sub-type - useful for screening for
agonists and antagonists and researching asthmatic diseases
This sequence encodes the protein of the invention. The protein of the
invention is a beta-2 adrenergic receptor subtype with kd value of
approximately 75 pM against 125I-cyopindrolol. The protein can be used in
assays for identifying agonists and antagonists, which are useful in researching
asthmatic diseases.

Sequence 1999 BP: 477 A: 513 C: 485 G: 524 T:
Query Match 0.0% Score 16: RESU38: length 1999;
Local Similarity 100% Score 4400;
Matches 16: Conservative 0: Mismatch 0: Indels 0: Gaps 0:

DD 529 gtcgtctgctcaccgg 544
Cp 1465 GTGCTGTGCTGACGG 1450

RESU38 50
ID Q39607 standard; cDNA, 2006 BP.
AC Q39607:
DT 16-MAR-1993 (first entry)
NA Human lung epithelial primary receptor clone,
PM PubMed; 125500000; Human lung epithelial primary receptor clone,
KM antibodies; hypercalcaemia; as
Homo sapiens.
Key Location/Qualifiers
FT 26
FT CDS
FT /tag= a
W09217602-A.
15-OCT-1992. U03821.
03-APR-1991: US-681702.
06-APR-1992: US-864475.
P (GENO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
P (GENO) Gen Hospital Corp Office Technology.
Suppl EVN
WP1: 92-366271(14).
New drug treating parathyroid hormone receptor: DNA and antibodies
for diagnosis and treatment of tumours associated with hypercalcaemia, and diagnosis
and treatment of tumours associated with hypercalcaemia, and diagnosis
Claim 5; Fig 6; 91pp: English.

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Search completed: Mon Nov 23 20:08:58 1998
Job time : 457 secs.

US-08-468-011A-2. rept

560	6	1.1	673	11	061592	GAS 6 MHA ASSOCIATED	1.57e+02
561	6	1.1	674	11	063772	GROWTH POTENTIATING FA	1.57e+02
562	6	1.1	674	11	060979	SKY/SINO RELATED (SNO P	1.57e+02
563	6	1.1	675	11	064741	SKY/SINO RELATED (SNO P	1.57e+02
564	6	1.1	675	11	064741	SKY/SINO RELATED (SNO P	1.57e+02
565	6	1.1	685	3	013439	UPL YLR143H	1.57e+02
566	6	1.1	689	5	016717	F22E5.15 PROTEIN.	1.57e+02
567	6	1.1	690	3	005951	SKI-RELATED ONCOGENE S	1.57e+02
568	6	1.1	692	4	005951	SKI-RELATED ONCOGENE S	1.57e+02
569	6	1.1	692	4	005951	SKI-RELATED ONCOGENE S	1.57e+02
570	6	1.1	693	4	005951	SKI-RELATED ONCOGENE S	1.57e+02
571	6	1.1	694	3	007261	K-TRANSFORMING GROWTH	1.57e+02
572	6	1.1	697	3	013335	RNA FROM CHROMOSOME X	1.57e+02
573	6	1.1	697	3	013335	RNA FROM CHROMOSOME X	1.57e+02
574	6	1.1	702	5	008649	NADH DEHYDROGENASE F	1.57e+02
575	6	1.1	703	6	028435	HYPERPHASE (6.4 KD P	1.57e+02
576	6	1.1	703	1	064698	POLI. HYPERPHASE (6.4 KD P	1.57e+02
577	6	1.1	703	1	064698	HYPERPHASE (6.4 KD P	1.57e+02
578	6	1.1	703	6	028437	CALPAIN, LARGE (CATALY	1.57e+02
579	6	1.1	703	6	028438	CALPAIN, LARGE (CATALY	1.57e+02
580	6	1.1	708	6	029539	ABC-TRANSPORTER.	1.57e+02
581	6	1.1	708	6	029539	ABC-TRANSPORTER.	1.57e+02
582	6	1.1	713	3	012643	ABC-TRANSPORTER.	1.57e+02
583	6	1.1	713	13	090330	LACTOPERIN PRECURSOR.	1.57e+02
584	6	1.1	715	10	023223	NEUTROPHILIC GRANULE STRA	1.57e+02
585	6	1.1	717	2	040557	HYDROLYTIC ENZYME	1.57e+02
586	6	1.1	727	2	040557	HYDROLYTIC ENZYME	1.57e+02
587	6	1.1	731	5	019355	PIROBLAST GROWTH FACT	1.57e+02
588	6	1.1	733	2	077833	HYPOPHYSICAL R1.4 KD P	1.57e+02
589	6	1.1	736	5	093238	MEIOGOCIN A TRANSLOCATO	1.57e+02
590	6	1.1	736	5	093238	MEIOGOCIN A TRANSLOCATO	1.57e+02
591	6	1.1	736	5	093238	MEIOGOCIN A TRANSLOCATO	1.57e+02
592	6	1.1	750	10	041003	CODED FOR BY G. ELEGANS	1.57e+02
593	6	1.1	767	4	092805	RNA POLYMERASE B10MA F	1.57e+02
594	6	1.1	767	4	092805	RNA POLYMERASE B10MA F	1.57e+02
595	6	1.1	772	10	021590	HYPOPHYSICAL PROTEIN F	1.57e+02
596	6	1.1	772	10	021590	HYPOPHYSICAL PROTEIN F	1.57e+02
597	6	1.1	773	5	019544	HYPOPHYSICAL X PRECURSOR	1.57e+02
598	6	1.1	776	5	019544	HYPOPHYSICAL X PRECURSOR	1.57e+02
599	6	1.1	776	5	019544	HYPOPHYSICAL X PRECURSOR	1.57e+02
600	6	1.1	781	14	014269	DNA TOPOISOMERASE I.	1.57e+02
601	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
602	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
603	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
604	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
605	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
606	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
607	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
608	6	1.1	786	2	094666	GOLDI COMPLEX AUTOMAT	1.57e+02
609	6	1.1	815	5	023860	HYPOPHYSICAL 93.7 KD P	1.57e+02
610	6	1.1	822	2	033831	HYPOPHYSICAL 93.7 KD P	1.57e+02

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611	6	1.1	837	3	043051	HYDROLYTIC 05.2 KD, P	1.57e-02
612	6	1.1	829	4	013488	SPECIFIC 116.0DA VACUO	1.57e-02
613	6	1.1	834	14	085065	2A INOLATE-XYLON OXIDO	1.57e-02
614	6	1.1	857	10	041238	LIPOINATE-XYLON OXIDO	1.57e-02
615	6	1.1	820	10	042726	HEAT SHOCK PROTEIN, E	1.57e-02
616	6	1.1	861	10	032507	LIPONASE, E (EC 1.1.3.	1.57e-02
617	6	1.1	861	10	032507	LIPONASE, E (EC 1.1.3.	1.57e-02
618	6	1.1	861	10	034379	LIPONASE, E (EC 1.1.3.	1.57e-02
619	6	1.1	861	10	023508	LIPONASE, E (EC 1.1.3.	1.57e-02
620	6	1.1	861	10	023508	LIPONASE, E (EC 1.1.3.	1.57e-02
621	6	1.1	864	10	043150	5-LIPONASE, E (EC 1.1.	1.57e-02
622	6	1.1	864	2	068395	GLYCINE FREE RADICAL, P	1.57e-02
623	6	1.1	874	5	001632	CODED FOR BY C. ELEGANS	1.57e-02
624	6	1.1	898	6	048525	PREDICTED PROTEIN.	1.57e-02
625	6	1.1	899	6	048525	PREDICTED PROTEIN.	1.57e-02
626	6	1.1	901	10	024585	CRINKLY 4 PRECURSOR.	1.57e-02
627	6	1.1	902	4	043632	SPINDEL POLE BODY PROT	1.57e-02
628	6	1.1	905	3	001966	C73A12. 9 PROTEIN., KD	1.57e-02
629	6	1.1	906	11	075586	NEURONAL-STOP PROTEIN.	1.57e-02
630	6	1.1	906	11	075586	NEURONAL-STOP PROTEIN.	1.57e-02
631	6	1.1	906	11	055129	STOP PROTEIN.	1.57e-02
632	6	1.1	911	2	048004	TRANSFERIN BINDING PR	1.57e-02
633	6	1.1	911	2	048004	TRANSFERIN BINDING PR	1.57e-02
634	6	1.1	913	2	048035	TRANSFERIN BINDING PR	1.57e-02
635	6	1.1	914	4	000291	HUNTINGTIN INTERACTING	1.57e-02
636	6	1.1	914	2	048039	TRANSFERIN BINDING PR	1.57e-02
637	6	1.1	927	2	037952	HPA1 GENE.	1.57e-02
638	6	1.1	927	2	037952	HPA1 GENE.	1.57e-02
639	6	1.1	942	6	095334	AMINOPEPTIDASE A, (EC 3	1.57e-02
640	6	1.1	949	5	090956	TOLD3. 3.	1.57e-02
641	6	1.1	952	11	063560	STOP PROTEIN.	1.57e-02
642	6	1.1	952	11	063560	STOP PROTEIN.	1.57e-02
643	6	1.1	970	2	065931	HYDROLYTIC 105.7 KD	1.57e-02
644	6	1.1	975	5	015743	SPALTIN.	1.57e-02
645	6	1.1	978	11	055097	PROXONASE ASSEMBLY FA	1.57e-02
646	6	1.1	981	4	087645	GLYCOPOLYMERASE, E (EC	1.57e-02
647	6	1.1	981	4	087645	GLYCOPOLYMERASE, E (EC	1.57e-02
648	6	1.1	989	5	018115	SIMILAR TO TRNA-PROCESS	1.57e-02
649	6	1.1	991	5	018152	T28B6. 4.	1.57e-02
650	6	1.1	991	5	018053	CHBER PROTOONCOGENE PR	1.57e-02
651	6	1.1	997	11	048005	CELLULAR SURFACE ANTIGEN	1.57e-02
652	6	1.1	999	4	012866	MAJOR SPROUT ANTIGEN	1.57e-02
653	6	1.1	1005	3	003794	LA PROTEIN.	1.57e-02
654	6	1.1	1006	4	085064	HYDROLYTIC 105.7 KD	1.57e-02
655	6	1.1	1006	4	085064	HYDROLYTIC 105.7 KD	1.57e-02
656	6	1.1	1036	5	019987	HYDROLYTIC 105.7 KD	1.57e-02
657	6	1.1	1029	4	069500	SARCO/ENDOPASMIC RETI	1.57e-02
658	6	1.1	1029	10	065590	RECEPTOR PROTEIN AIMS	1.57e-02
659	6	1.1	1038	13	044360	RANBP7. PROTEIN.	1.57e-02
660	6	1.1	1038	13	044360	RANBP7. PROTEIN.	1.57e-02
661	6	1.1	1039	10	023792	PAF9.15 PROTEIN.	1.57e-02

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662	6	1,1	1042	1	050295	PURATIVE TUB. II RESTRI	157+02
663	6	1,1	1046	11	055156	CLIP-115 PROTEIN	157+02
664	6	1,1	1049	10	P93762	SUCROSE-PROPHATE SYNT	157+02
665	6	1,1	1049	10	Q43802	SUCROSE-PROPHATE SYNT	157+02
666	6	1,1	1051	2	Q30776	GLYCOPROTEIN BINDING	157+02
667	6	1,1	1051	2	Q30776	HYDROLYSIS GALLICACID	157+02
668	6	1,1	1060	5	Q93804	HEPATOCT. 2.	157+02
669	6	1,1	1067	10	Q23159	AMINOACET. T-RNA SYNTH	157+02
670	6	1,1	1067	10	Q23159	SUCROSE-PROPHATE SYNT	157+02
671	6	1,1	1081	10	Q64933	INTEGRIN	157+02
672	6	1,1	1084	10	Q43010	SUCROSE-PROPHATE SYNT	157+02
673	6	1,1	1086	5	Q18428	CONJUG. HYDROXYLACETYL	157+02
674	6	1,1	1086	5	Q18428	CONJUG. FASII.	157+02
675	6	1,1	1099	5	Q20073	COSMID 43 PROTEIN.	157+02
676	6	1,1	1106	5	Q16310	COS28.4 PROTEIN.	157+02
677	6	1,1	1108	10	Q42821	P22K20.5 PROTEIN.	157+02
678	6	1,1	1109	10	Q64512	WTR. RETRANSDUCTION LI	157+02
679	6	1,1	1129	9	Q64512	WTR. RETRANSDUCTION LI	157+02
680	6	1,1	1125	5	P92135	GAL/GALACT. LECTIN HEAV	157+02
681	6	1,1	1131	10	Q23159	CU2A-TRANSPORTING ATPA	157+02
682	6	1,1	1139	4	Q12371	GLYCOPROTEIN PRECURSOR	157+02
683	6	1,1	1140	5	Q64311	VAL. TERN. SYNTHASE.	157+02
684	6	1,1	1165	2	Q67411	VAL. TERN. SYNTHASE.	157+02
685	6	1,1	1175	4	Q13632	NPAT.	157+02
686	6	1,1	1183	5	Q18080	SIMILAR TO HUMAN MELT1	157+02
687	6	1,1	1183	5	Q18080	PROBABLE SYNTHASE (P	157+02
688	6	1,1	1213	3	Q47072	ADP-BINDING CASSETTE (157+02
689	6	1,1	1218	2	P96057	ADP-BINDING CASSETTE (157+02
690	6	1,1	1218	11	Q70365	COLGAIN-245.	157+02
691	6	1,1	1218	11	Q70365	ENVELOPE POLYPROTEIN	157+02
692	6	1,1	1218	11	Q70365	ENVELOPE POLYPROTEIN	157+02
693	6	1,1	1243	9	Q93934	GENE 37 FOR RECEPTOR R	157+02
694	6	1,1	1245	4	Q88432	STRUCTURAL POLYPROTEIN	157+02
695	6	1,1	1245	4	Q88430	STRUCTURAL POLYPROTEIN	157+02
696	6	1,1	1245	4	Q88430	STRUCTURAL POLYPROTEIN	157+02
697	6	1,1	1261	11	Q64621	RECEPTOR-LINKED PROTEI	157+02
698	6	1,1	1264	5	P93767	NEUROGLIAN.	157+02
699	6	1,1	1273	5	Q49288	SAX-3.	157+02
700	6	1,1	1273	5	Q49288	SAX-3.	157+02
701	6	1,1	1290	2	Q06021	VACUOLATING CYTOCHIN	157+02
702	6	1,1	1297	5	Q26632	PROTEOLIAISIN (PRAGHEN	157+02
703	6	1,1	1319	4	Q66609	TEGUMENT PROTEIN.	157+02
704	6	1,1	1353	13	Q44103	PEPTIDE-SYNTHASE (FR	157+02
705	6	1,1	1353	13	Q44103	PEPTIDE-SYNTHASE (FR	157+02
706	6	1,1	1354	4	Q13464	RHO-ASSOCIATED, COILED-	157+02
707	6	1,1	1354	11	P70335	RHO-ASSOCIATED, COILED-	157+02
708	6	1,1	1359	11	Q17822	PS9B11.1.	157+02
709	6	1,1	1369	11	Q17822	PS9B11.1.	157+02
710	6	1,1	1374	14	P88442	MAJOR CAPSID PROTEIN.	157+02
711	6	1,1	1385	5	P93389	SIMILARITY TO SIVERAL.	157+02
712	6	1,1	1388	13	Q93785	KLP2 PROTEIN.	157+02

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6	1.1	1404	5	001363	CELF35-1.	1.57e-02
6	1.1	1427	4	001363	CELF35-1.	1.57e-02
6	1.1	1427	4	012007	E14. PROTEIN	1.57e-02
6	1.1	1441	5	026453	HLS-ROSENLESS (FRAGMENT	1.57e-02
6	1.1	1457	5	026627	SPERM RECEPTOR FOR EGG	1.57e-02
6	1.1	1457	5	026627	SPERM RECEPTOR FOR EGG	1.57e-02
6	1.1	1458	5	001644	CHROMOSOME XII COXII	1.57e-02
6	1.1	1454	3	006164	CHROMOSOME XII COXII	1.57e-02
6	1.1	1455	5	017012	R13D1.1.7 PROTEIN.	1.57e-02
6	1.1	1462	10	006035	RETROVIRUS-RELATED POL	1.57e-02
6	1.1	1462	10	006035	RETROVIRUS-RELATED POL	1.57e-02
6	1.1	1466	5	048084	PI42D.8 PROTEIN.	1.57e-02
6	1.1	1466	5	048084	PI42D.8 PROTEIN.	1.57e-02
6	1.1	1495	11	007808	PROTEIN-TYROSINE PHOSP	1.57e-02
6	1.1	1499	13	030815	PROTEIN-TYROSINE PHOSP	1.57e-02
6	1.1	1499	13	030815	PROTEIN-TYROSINE PHOSP	1.57e-02
6	1.1	1501	5	024298	DR-CANDLER, RII	1.57e-02
6	1.1	1507	5	024298	DR-CANDLER, RII	1.57e-02
6	1.1	1526	5	079669	MYOSIN II.	1.57e-02
6	1.1	1534	5	026946	P-GLYCOPROTEIN.	1.57e-02
6	1.1	1534	5	026946	P-GLYCOPROTEIN.	1.57e-02
6	1.1	1559	9	002066	KLK10/330 PROTEIN (FNA3	1.57e-02
6	1.1	1559	9	002066	KLK10/330 PROTEIN (FNA3	1.57e-02
6	1.1	1642	4	014859	YOTAAO.	1.57e-02
6	1.1	1661	10	023557	HYPOTHETICAL 1.85.0 ND	1.57e-02
6	1.1	1690	5	049328	MICROTUBULE BINDING PR	1.57e-02
6	1.1	1690	5	049328	MICROTUBULE BINDING PR	1.57e-02
6	1.1	1805	4	029545	WELSHL28 KIAA0257 (P	1.57e-02
6	1.1	1805	4	029545	WELSHL28 KIAA0257 (P	1.57e-02
6	1.1	1805	11	036361	FISHER 344 PR4-SILAM0	1.57e-02
6	1.1	1814	11	061037	TUBERIN (TUBEROUS SCLE	1.57e-02
6	1.1	1814	11	061037	TUBERIN (TUBEROUS SCLE	1.57e-02
6	1.1	1819	5	044436	MANUBRIAN C-5-PEPTIDE	1.57e-02
6	1.1	1831	4	044436	MANUBRIAN C-5-PEPTIDE	1.57e-02
6	1.1	1863	11	064605	LEUKOCYTE COMMON ANTIG	1.57e-02
6	1.1	1898	5	064490	PROSPHOLIPASE C PIC210	1.57e-02
6	1.1	1907	11	064605	PROSPHOLIPASE C PIC210	1.57e-02
6	1.1	1911	4	044436	PROSPHOLIPASE C PIC210	1.57e-02
6	1.1	1911	4	015718	PP25A3A PRECURSOR (EC	1.57e-02
6	1.1	1922	5	039936	F13B1.2.	1.57e-02
6	1.1	1928	4	039735	RESCN1 (FRAGMENT).	1.57e-02
6	1.1	1928	4	039735	RESCN1 (FRAGMENT).	1.57e-02
6	1.1	1934	5	039548	PROTEIN-TYROSINE PHOSP	1.57e-02
6	1.1	1934	5	039548	PROTEIN-TYROSINE PHOSP	1.57e-02
6	1.1	1965	5	061893	TOH18.4 PROTEIN	1.57e-02
6	1.1	1965	5	061893	TOH18.4 PROTEIN	1.57e-02
6	1.1	1966	4	060840	L-TYPE CALCIUM CHANNEL	1.57e-02
6	1.1	1968	4	039548	ORP1.22K PROTEIN.	1.57e-02
6	1.1	1968	4	039548	ORP1.22K PROTEIN.	1.57e-02
6	1.1	2004	3	02104	MYOSIN II. ISOFORM, HEAV	1.57e-02
6	1.1	2109	4	037899	TFIIIC BOX B-BINDING S	1.57e-02
6	1.1	2127	4	057294	L. PROTEIN, RNA DEPENDE	1.57e-02
6	1.1	2127	4	057294	L. PROTEIN, RNA DEPENDE	1.57e-02
6	1.1	2183	14	064952	TRANS-GLUTAMINATION FA	1.57e-02
6	1.1	2183	14	064952	TRANS-GLUTAMINATION FA	1.57e-02
6	1.1	2207	4	039555	PWJ POLYPROTEIN	1.57e-02
6	1.1	2251	5	022150	TO5A10.1.	1.57e-02
6	1.1	2251	5	022150	TO5A10.1.	1.57e-02
6	1.1	2271	4	039548	F13B1.2.	1.57e-02
6	1.1	2271	4	039548	F13B1.2.	1.57e-02
6	1.1	2325	4	039675	MELANOMA-ASSOCIATED CH	1.57e-02
6	1.1	2325	4	039675	MELANOMA-ASSOCIATED CH	1.57e-02
6	1.1	2351	10	023372	HYPOTHETICAL PROTEIN.	1.57e-02
6	1.1	2351	10	023372	HYPOTHETICAL PROTEIN.	1.57e-02

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968	5	0	9	859	3	004048	D9461.6P
969	5	0	9	865	1	027595	FORMATE DEHYDROGENASE,
970	5	0	9	869	4	000213	SUB1.5 MRNA.
971	5	0	9	901	2	072250	CHET-1
972	5	0	9	907	3	004234	CHET-1
973	5	0	9	967	3	004234	CHROMOSOME XV READING E
974	5	0	9	968	2	025923	TYPE III RESTRICTION E
975	5	0	9	979	1	052003	SIMILAR TO ESCHERICHIA
976	5	0	9	979	1	052003	SIMILAR TO ESCHERICHIA
977	5	0	9	979	1	052003	CAPACITATIVE CALCIUM E
978	5	0	9	1001	3	027100	ADENOSINE PHOSPHATE
979	5	0	9	1046	5	044316	REVERSE TRANSCRIPTASE
980	5	0	9	1136	5	027806	DYNEIN HEAVY CHAIN ISO
981	5	0	9	1146	2	067037	REVERSE GYRASE.
982	5	0	9	1159	2	053750	ADENOSINE PHOSPHATE
983	5	0	9	1226	3	006836	REVERSE TRANSCRIPTASE
984	5	0	9	1250	5	023409	SIMILARITY TO TIPA.
985	5	0	9	1275	2	023016	CSM5MD K11393.
986	5	0	9	1285	2	023016	CSM5MD K11393.
987	5	0	9	1534	4	015249	HYDROLYTIC-153.1 KD
988	5	0	9	1613	5	044368	POE DOMAIN PROTEIN.
989	5	0	9	1626	3	042838	GENETICS KHAN.
990	5	0	9	1636	3	042838	RETROTRANSPONSON T15-6P
991	5	0	9	2166	2	051465	HYDROLYTIC-25A.2 KD
992	5	0	9	2185	4	014436	256.6 KD GOLGIN.
993	5	0	9	2210	3	014581	RETROTRANSPONSON T15-6P
994	5	0	9	2218	2	063718	HYDROLYTIC-25A.2 KD
995	5	0	9	2748	2	063718	HYDROLYTIC-25A.2 KD
996	5	0	9	2500	5	020937	ADENOSINE PHOSPHATE
997	5	0	9	2685	3	014151	SIMILAR TO S.
998	5	0	9	3229	5	025912	HYDROLYTIC-110.3 KD
999	5	0	9	3229	5	025912	PROTEIN 1 OF A DISPERS
1000	5	0	9	3654	2	030766	POLYKETIDE SYNTHASE MO

ALIGNMENTS

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5. RESULT

Db 353 SFGFFVS 360
QY 403 SFGFFVS 410

RESULT 7 PRELIMINARY: PRT: 438 AA.
ID Q3768
AC Q3768
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE GROWTH-HORMONE-RELEASING HORMONE-LIKE PEPTIDE RECEPTOR.
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, PISCES, GNATHOSTOMATA.
OC OSTEICHTHES, ACTINOPTERYGII, CYPRINIFORMES.
RN [1] SEQUENCE FROM N.A.
RA CHAN K.W. YU K., RIVIER J., CHOW B.K.C.;
RL NEUROENDOCRINOLOGY 0:0-0(1998).
DR ENBL: AF048819; G3098567;
SQ SEQUENCE 438 AA: 50305 MW: 869907076 CRC32:
Query Match 1.58; Score 8; DB 13; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.67e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 165 HCTNRVH 172
QY 173 HCTNRVH 180

RESULT 8 PRELIMINARY: PRT: 1904 AA.
ID Q3819
AC Q3819
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE ORF1904.
OC BACTERIOPHAGE B5-T.
OC VIRIDAE, NONCLASSIFIED VIRUSES.
RN [1] SEQUENCE FROM N.A.
RA BOYCE J.D., DAVIDSON B.E., HILLIER A.J.;
RL APPL. ENVIRON. MICROBIOL. 0:0-0(0).
RN [2] SEQUENCE FROM N.A.
RA BOYCE J.D., DAVIDSON B.E., HILLIER A.J.;
RL APPL. ENVIRON. MICROBIOL. 0:0-0(0).
RN [3] SEQUENCE FROM N.A.
RA BOYCE J.D., DAVIDSON B.E., HILLIER A.J.

(1) SEQUENCE FROM N.A.
RN STRAIN-H37RV.
RC SUBMITTED (MAR-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
(2) SEQUENCE FROM N.A.
RN STRAIN-H37RV.
RC SUBMITTED (MAR-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
(3) SEQUENCE FROM N.A.
RN STRAIN-H37RV.
RC SUBMITTED (MAR-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
RN PHILIPP N.J., POULET S., EIGMEIER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERCH S., BLOOM S.R., JACOBS W.R. JR.,
CODE S.T.; ACAD. SCI. U.S.A. 93:3132-3137(1996).
DR ENBL: AL021211; E1264515;
KM HYPOTHETICAL PROTEIN
SQ SEQUENCE 125 AA: 13007 MW: CA70020C CRC32:
Query Match 1.31; Score 7; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.22e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 9 TLVVLV 15
QY 365 TLVVLV 371

RESULT 11 PRELIMINARY: PRT: 164 AA.
ID Q58113
AC Q58113
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE 164-AMONG HYPOTHETICAL PROTEIN.
GN PRAB004
OS PYROCOCCUS HORIKOSHII.
OC ARCHAEA: EURYARCHAEOTA, THERMOCOCCALES; PYROCOCCUS.
RN [1] SEQUENCE FROM N.A.
RA KANARABASI Y., SHAWA M., HORIYAMA H., HATAKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSIYAMA A., NAGAI Y.,
RA FUNAHASHI O., TANAKA T., KUDOH T., KAWANAKA K., OHFUCHI A.,
RA AKI K., YOSHISAWA T., NAKAMURA Y., MASUCHI Y., SHIOTA H., KINUCHI R.;
RL SUBMITTED (DEC-1997) TO ENBL/GENBANK/DBJ DATA BANKS.
DR ENBL: AB009484; D1027696;

RL APPL. ENVIRON. MICROBIOL. 3:0-0(0).
DR ENBL: L4593; G928828;
SQ SEQUENCE 1904 AA: 204786 MW: ED9245B CRC32:
Query Match 1.58; Score 8; DB 9; Length 1904;
Best Local Similarity 100.0%; Pred. No. 1.67e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1773 SFGFFVS 1780
QY 403 SFGFFVS 410

RESULT 9 PRELIMINARY: PRT: 116 AA.
ID Q52161
AC Q52161
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 12.6 KD PROTEIN.
OC PSEUDOMONAS SYRINGAE.
OC PROKARYOTA, GRACILICUTES; SCOTOBACTERIA, AEROBIC RODS AND COCCI;
RN [1] PSEUDOMONADACEAE.
RN [2] SEQUENCE FROM N.A.
RA STRAIN-SUPP27.
RC SUBMITTED (JAN-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
DR ENBL: AF023808; G2716143;
KM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 116 AA: 12609 MW: D881152C CRC32:
Query Match 1.33; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.22e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 107 KPSRPM 113
QY 528 KPSRPM 534

RESULT 10 PRELIMINARY: PRT: 125 AA.
ID Q69623
AC Q69623
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 13.0 KD PROTEIN.
GN MYO25.003C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC PROKARYOTA, FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.

SQ SEQUENCE 164 AA: 19056 MW: F7BD25C6 CRC32:
Query Match 1.33; Score 7; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 2.22e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 96 GFVSII 102
QY 406 GFVSII 412

RESULT 12 PRELIMINARY: PRT: 166 AA.
ID Q53670
AC Q53670
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DE HYPOTHETICAL 18.1 KD PROTEIN.
OS ESCHERICHIA COLI.
OC PROKARYOTA, GRACILICUTES; SCOTOBACTERIA, FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1] SEQUENCE FROM N.A.
RA WANG Y.-D., ZHAO S., HILL C.W.;
RL SUBMITTED (JAN-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
DR ENBL: AF045039; G2920642;
KM HYPOTHETICAL PROTEIN.
SQ SEQUENCE 166 AA: 18051 MW: 79957757 CRC32:
Query Match 1.33; Score 7; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.22e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 71 AALGNF 77
QY 324 AALGNF 330

RESULT 13 PRELIMINARY: PRT: 190 AA.
ID P73050
AC P73050
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DE FERROPOCHELIN BINDING PROTEIN.
OC SYNCHOCYSTIS SP.
OC EUBACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNCHOCYSTIS.
RN [1]

[illegible]

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RA JONESTON M., WILLER T., RILES L., ALBERMANN K., ANDRE B., ANSOERKE W.,
RA BENSE V., BRUCKNER M., DELIUS L., DUBOIS E., DUGTENHOFF A.,
RA ERTIAN K.D., FLOERCH M., COFFEAU A., HELZLING U., HEUMANN K.,
RA HEISE-KITTEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,
RA KUEHN M., KUEHN M., KUEHN M., KUEHN M., KUEHN M., KUEHN M.,
RA MULLER-AUER G., NERNWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
RA PORTIELLE D., FERNELLE B., REICHMAN S., RIEGER M., RINKE M., ROSE M.,
RA SCHAPE M., SCHREIBS B., SCHOLLER P., SCHWAGER C., SCHWAB S.,
RA SCHWAB S., SCHWAB S., SCHWAB S., SCHWAB S., SCHWAB S., SCHWAB S.,
RA VIERDEL P., VOET V., VOLKART G., VOSS R., WAKELAND W., WEDLER Z.,
RA WEDLER Z., ZIMMERMAN F.K., ZOLLNER A., NANI J., HOREISEL J.D.,
RA NATURE 387: 0-0(0).
RL SEQUENCE FROM N.A.
RS SEQUENCE FROM N.A.
RC STRAIN=2688C (AS972);
RC DU 2.;
RL RC
RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDJB DATA BANKS.
RL SEQUENCE FROM N.A.
RC STRAIN=2688C (AS972);
RC WATSONSON R.;
RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDJB DATA BANKS.
RL SEQUENCE FROM N.A.
RC STRAIN=2688C (AS972);
RC CHERRY J.M.;
RA SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDJB DATA BANKS.
RL SEQUENCE FROM N.A.
RL DU 2688C (AS972);
RL SEQUENCE 229 AA 25686 MW; 4E7F5346 CRC32;
Query Match 1.3%; Score 7; DB 3; Length 229;
Percent Local Similarity 100.0%; P-Val 6.22e-007;
Machine %; Generalizable 0; Mutations 0; Indels 0; Gaps 0;
DB 105 TAGSITS 111
QY 503 INSHSLD 509
RESULTS 17
ID 2688C PRELIMINARY; PRT: 239 AA.
CD P94837
AT 01-MAY-1997 (TREMBLAEZ_03, CREATED)
DT 01-MAY-1997 (TREMBLAEZ_03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLAEZ_03, LAST ANNOTATION UPDATE)
DE ALPHA-RESPOLIANTIN (ALPHA-RESPOLIANTIN)
DE ALPHARESPOLIANTIN (ALPHARESPOLIANTIN)
DE (AMINOCARBOXYMATE-SEMIALDEHYDE DECARBOXYLASE).
GN ALSD
GN GENOCOCUS OBN1
GN GENOCOCUS OBN1
GN LACTOBACILLACEAE, GENOCOCUS
OC LACTOBACILLACEAE, GENOCOCUS

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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	Db	Qy	RESULT	15	PRT:	210 AA.
			ID	O64625		
			DT	01-AUG-1988 (TREMLJLAEI, 07, CREATED)		
			DT	01-AUG-1988 (TREMLJLAEI, 07, LAST SEQUENCE UPDATE)		
			DT	01-AUG-1988 (TREMLJLAEI, 07, LAST ANNOTATION UPDATE)		
			GN	F18P74 IS PROTEIN.		
			OS	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).		
			OC	EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONAE;		
			CC	(CAPNARIACEAE; CRUCIFERAE.		
			RP	SEQUENCE FROM N.A.		
			RC	STRAIN-CV. COLOMBIA;		
			RA	RONSELEY S.D., LIN X.; KETCHUM K.A., CROSSBY M.L., BRANDON R.C.,		
			RE	WILSON J.E., HENRIKSEN L.H., KERNLAUGE A.R., ADAMS H.O.,		
			RL	SOMMERVILLE C.D., VENTER J.C.,		
			BA	SUBMITTED (APR-1998) TO EMBL/GEMBL/DDJB DATA BANKS.		
			DR	EMBL, AC001673: G3004556; -		
			SQ	SEQUENCE 210 AA; 21161 MW; 0BD7JA25 CRC32:		
				Best Match	1.3%; Score by: DB 10; Length 210;	
				Query Local Similarity 100.0%; Pred. No. 2,22e+00;		
			Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
			Db	100 LFVSPNL 106		
			Qy	183 LFVSPNL 189		

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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	Db	Qy	RESULT	16	PRT:	229 AA.
			ID	Q06070		
			AC	O06070; 1996 (TREMLJLAEI, 01, CREATED)		
			DT	01-NOV-1996 (TREMLJLAEI, 01, LAST SEQUENCE UPDATE)		
			DT	01-AUG-1998 (TREMLJLAEI, 07, LAST ANNOTATION UPDATE)		
			DE	CHROMOSOME XII COSMID 8084.		
			NB	SCHWARZWEISS CERVISIAR (BAKER'S YEAST).		
			GN	SCHWARZWEISS CERVISIAR (BAKER'S YEAST).		
			OC	EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOWCETES.		
			RP	SEQUENCE FROM N.A.		
			RC	STRAIN-CV. COLOMBIA;		
			RA	RONSELEY S.D., LIN X.; KETCHUM K.A., CROSSBY M.L., BRANDON R.C.,		
			RE	WILSON J.E., HENRIKSEN L.H., KERNLAUGE A.R., ADAMS H.O.,		
			RL	SOMMERVILLE C.D., VENTER J.C.,		
			BA	SUBMITTED (APR-1998) TO EMBL/GEMBL/DDJB DATA BANKS.		
			DR	EMBL, AC001673: G3004556; -		
			SQ	SEQUENCE 210 AA; 21161 MW; 0BD7JA25 CRC32:		
				Best Match	1.3%; Score by: DB 10; Length 210;	
				Query Local Similarity 100.0%; Pred. No. 2,22e+00;		
			Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
			Db	100 LFVSPNL 106		
			Qy	183 LFVSPNL 189		

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[1]
NW      SEQUENCE FROM N.A.
RP
RC      STRAIN-LO 84.13.
RC      MEDLINE: 97132647.
RC      MEDLINE: 97132647.
RC      P1: MARTINEAU, B., GUEZO, J., CAVIN J.F., DIVIES C.:
RC      "PLASMA MICROBIAL ACTIVITY: 2-AMINO-3-(3-OXOPROP-2-ENYL)-BUT-2-ENEDIAMIDE + CO(2)".
RC      CATALYTIC ACTIVITY: 2-AMINO-3-(3-OXOPROP-2-ENYL)-BUT-2-ENEDIAMIDE + CO(2).
CC      EMBL: X93091: E214715: -.
DR
SQ      SEQUENCE 239 AA: 26746 MW: 6F6E2065 CRC32:
      Query Match      1.3%; Score 7; DB 2; Length 239;
      Best Local Similarity 100.0%; Pred No. 2, 22e+00;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      152 ADSLTA1 158
Qy      483 ADSLTA1 489
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RESULT 18
ID      O68899
AC      1-AUG-1998 (TREMBL)
DT      01-AUG-1998 (TREMBL) 07, CREATED
DT      01-AUG-1998 (TREMBL) 07, LAST SEQUENCE UPDATE
DT      01-AUG-1998 (TREMBL) 07, LAST ANNOTATION UPDATE)
DE      HYPOPHYSICAL 29.5 KD PROTEIN (CAMPYLOBACTER PYLORI).
OE      PLASMIN PIPRO 00
OG      PROKARYOTA: GRACILICUTES: SCOTOBACTERIA:
OC      AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
RC      SEQUENCE FROM N.A.
RC      STRAIN-OUI45B.
RA      CHU C.-S., CHOW H.-P., OU J.T.:
RA      EMBL: M25049: 12914602
RA      EMBL: M25049: 12914602
KW      HYPOPHYSICAL PROTEIN: PLASMIN.
SQ      SEQUENCE 252 AA: 29476 MW: 3CAF8FC5 CRC32:
      Query Match      1.3%; Score 7; DB 2; Length 252;
      Best Local Similarity 100.0%; Pred No. 2, 22e+00;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      161 SEUNSL1 167
Qy      485 SEUNSL1 491
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RW      NATURE 369:32-38(1994).
RW      [2]
RC      SEQUENCE FROM N.A.
RC      STRAIN=GRISTOL N2;
RA      STRAIN=Y. HUTCHINSON P., BEK C.;
RW      SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDJ DATA BANKS.
RW      [3]
RC      SEQUENCE FROM N.A.
RC      STRAIN=GRISTOL N2;
RA      STRAIN=Y. HUTCHINSON P., BEK C.;
RW      SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDJ DATA BANKS.
RW      ZMEL: AF046420; G2291176; -.
RC      SEQUENCE 291 AA: 34059 MW: 5413BC06 CRC32:
RW      Query Match
RW      Best Local Similarity 100.0%; Pred. No. 2,226+00;
RW      Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB      122 LFVSPML 128
QY      183 LFVSPML 189
          |||||
RESULT   21    PRELIMINARY:      PRG: 351 AA.
AC       052572: 1998 (TREBLESL 06. CREATED)
AT       01-JUN-1998 (TREBLESL 07. LAST ANNOTATION UPDATE)
CT       01-AUG-1998 (TREBLESL 07. LAST ANNOTATION UPDATE)
DE       CYTOCHROME P450 MONOOXYGENASE.
DS       AMYCATALOPSIS MEDITERANEI.
OS       ACTINOMYCETES; ACTINOMYCETES; PSEUDONOCARDIACEAE;
OC       AMYCATALOPSIS.
QC       [1]
RR       RC      SEQUENCE FROM N.A.
RR       RC      STRAIN=5659;
RR       RL      KING C.G., YU T.W., FYHLE C., HANDA S., FLOSS H.G.;
RR       RL      J. BIOL. CHEM. 0:0-0(1998).
RR       [2]
RR       RC      SEQUENCE FROM N.A.
RR       RC      AUGUST P.R., TANG L., YOON Y.J., NIANG S., KOTTELLER R., YU T.W.,
RR       RA      TAYLOR M., ROFFMAN D., KIM C.G., ZHANG X., HUTCHINSON C.R.,
RR       RA      FLOSS H.G.:
RR       RL      GEN. BIOL. 5:0-0(0002).
RR       [3]
RR       RC      SEQUENCE FROM N.A.
RR       RC      STRAIN=5659;
RR       RA      AUGUST P.R., TANG L., YOON Y.J., NIANG S., KOTTELLER R., HUTCHINSON C.R.,
RR       RW      SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDJ DATA BANKS.

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06 TRYPAFNOGWA GUTHRIE.
07 EUTAROTIA ANTHILIN. PROTOGIA: SARCONASTIGOPHORA: HASTIGOPHORA:
08 ZOONASTIGOPHORA: KINETOPLASTIDA: TRYPAKOSCHATINA: TRYPAKOSMATIDE.
09
10 [1]
11 SEQUENCE FROM N.A.
12 DO TH. C. A. AERTS D., 1972.
13 DO TH. C. A. AERTS D., STEINERT M., PAYS E.:
14 EMBL. BIOCHEM. PARASITOL. 48:199-210(1991).
15 DBL. M62631: G152063: -
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[illegible][illegible]

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01-ANU-1998 (TREHLELZEL 07, LAST ANNOTATION UPDATE);
DB Z65.6 PROTEIN.
GN CAENORHABDITIS ELIGANS.
NC LUTARIVOTA; METAZOA; ACCELONATES; NEMATOIDA; SECERNENTEA; RHABDITIDA.
PP STRAIN-BRISTOL N2.
RC MEDLINE; 94150718.
RX SEQUENCE FROM N.A.
RA BONFIELD J., BURTON J., ANDERSON K., BAYNES C., BEERS M., COULSON A., CRATON M., DEAN S., DU Z., DUREN R., FAVELLO A., FULTON L., GARDNER A., GREENE K., HAKINS T., HILLIER L., JETER M., JOHNSTON L., LIGHTNING J., LEOPOLD C., MCCREARY A., McRTOMORE W., REEDS P., REID L., ROBINSON J., PERCY C., RIFKIN L., ROOPER A., SAUNDERS D., SHONKEEN R., PARSONS J., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., SALDON N., SMITH A., WINTER-HIGGS J., YOUNG I., WILKINSON-SPOFFORD J., WOODLAND P., WATERSTON R., VAUDIN M., VANOUGH K., WATERSTON R., WATSON R., WILKINSON-SPOFFORD J., WOODLAND P., NATURE 368:32-38(1994). [2]
RL SUBMITTED (MAY-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
RP NC STRAIN-BRISTOL N2.
RC NC STRAIN-BRISTOL N2.
RL SUBMITTED (MAY-1998) TO ENBL/GENBANK/DBJ DATA BANKS. [3]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RA WATERSTON R.;
RL SUBMITTED (MAY-1998) TO ENBL/GENBANK/DBJ DATA BANKS.
RL ENBL AP067942; G1616580;
DR ENBL AP067942; G1616580; 435 AA; 43145 BW; 283PCF78 CRC32;
Query Match 1.38; Score ?; DB 5; Length 435;
Best Local Similarity 100.0%; Fred No. 2.2e+00;
Matches ?; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 316 GSVALTY 322
Qy 449 GSVALTY 455
RESULT 27
ID O1012 PRELIMINARY; PRY: 448 AA.
DT DT 01-JAN-1998 (TREHLELZEL 05, CREATED)
DT DT 01-JAN-1998 (TREHLELZEL 05, LAST SEQUENCE UPDATE)
DT DT 01-JAN-1998 (TREHLELZEL 05, LAST ANNOTATION UPDATE)
OC VIRIBIO AGULLUNUM.
OC PSORAVOTIA; GRACILLICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;

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[illegible]

WPPQLH (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Nov 23 13:40:46 1998; MacPar time 13.64 seconds
Tabular output not generated.

Title: >US-08-468-011A-2
Description: (1-541) from US08468011A.ppt
Sequence: 1 NAWGASLHWGMLGSL.....DDLKMKSPRNSPTDQ 541

Scoring table: TABLE uniprottable

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 04
Listing first 1000 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 3.824; Variance 0.403; scale 9.499

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description	Pred. No.
1	413	76.3	550	PTR2_HUMAN PARATHYROID HORMONE RE	0.00e+00

53	7	1.3	360	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
54	7	1.3	360	1	MBHE_ALCEU	UPTAKE HYDROGENASE SNA	1.41e+00
55	7	1.3	360	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
56	7	1.3	360	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
57	7	1.3	378	1	SIG1_YEAST	SIG1 PROTEIN PRECURSOR	1.41e+00
58	7	1.3	395	1	DHP_PANSE	DIURETIC HORMONE RECP	1.41e+00
59	7	1.3	426	1	HML_AACH	GLUTAMYL-TRNA REDUCTAS	1.41e+00
60	7	1.3	426	1	HML_AACH	GLUTAMYL-TRNA REDUCTAS	1.41e+00
61	7	1.3	461	1	U45_LACIA	SECRETED 45 KD PROTEIN	1.41e+00
62	7	1.3	459	1	YB8_YEAST	HYPOTHETICAL 48.3 KD P	1.41e+00
63	7	1.3	564	1	MERA_SHIFL	MERCURIC REDUCTASE (EC	1.41e+00
64	7	1.3	628	1	ICAL_MOUSE	VASCULAR CELL ADHESION	1.41e+00
65	7	1.3	628	1	ICAL_MOUSE	VASCULAR CELL ADHESION	1.41e+00
66	7	1.3	1189	1	SC11_CHICK	CHROMOSOME SCAFFOLD PR	1.41e+00
67	7	1.3	1203	1	XCPE_XENLA	CHROMOSOME ASSEMBLY PR	1.41e+00
68	7	1.3	1339	1	DPOA_TREBB	DNA POLYMERASE ALPHA (1.41e+00
69	7	1.3	1398	1	YB8_YEAST	SECRETED 45 KD PROTEIN	1.41e+00
70	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
71	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
72	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
73	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
74	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
75	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
76	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
77	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
78	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
79	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
80	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
81	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
82	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
83	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
84	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
85	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
86	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
87	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
88	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
89	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
90	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
91	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
92	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
93	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
94	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
95	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
96	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
97	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
98	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
99	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
100	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
101	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
102	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00
103	6	1.1	1098	1	MBHE_RHOGE	UPTAKE HYDROGENASE SNA	1.41e+00

104	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
105	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
106	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
107	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
108	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
109	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
110	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
111	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
112	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
113	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
114	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
115	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
116	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
117	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
118	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
119	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
120	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
121	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
122	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
123	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
124	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
125	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
126	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
127	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
128	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
129	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
130	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
131	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
132	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
133	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
134	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
135	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
136	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
137	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
138	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
139	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
140	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
141	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
142	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
143	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
144	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
145	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
146	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
147	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
148	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
149	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
150	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
151	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
152	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
153	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01
154	6	1.1	184	1	YPS2_SYNP2	HYPOTHETICAL 20.9 KD P	9.71e-01

US-06-469-0111a-2.rep	6	1..1	261	1	Y152_MCTU	HYPOTHETICAL 26.9 KD P	9	71e+01
155	6	1..1	262	1	NARG_BAC50	NARGO PROTEIN.	9	71e+01
156	6	1..1	263	1	PLSC_MCPN	PUTATIVE 1-ACVLT-SN-GLY	9	71e+01
157	6	1..1	264	1	GLYS_MCPN	GLYCOSYLTRANSFERASE PH4 PREC	9	71e+01
158	6	1..1	265	1	GLYS_MCPN	GLYCOSYLTRANSFERASE PH4 PREC	9	71e+01
159	6	1..1	270	1	TSNR_STRU1	23S RRNA METHYLTRANSFERASE	9	71e+01
160	6	1..1	271	1	TSNR_STRU2	23S RRNA METHYLTRANSFERASE	9	71e+01
161	6	1..1	277	1	F23A_VTBP4	HYPOTHETICAL PROTEIN M	9	71e+01
162	6	1..1	284	1	F23A_VTBP4	LATERAL FLAGELLIN	9	71e+01
163	6	1..1	285	1	FLAA_VTBP4	FLAGELLIN	9	71e+01
164	6	1..1	286	1	SSYS_HUMAN	TRANSLOCOSOMAL PROTEIN	9	71e+01
165	6	1..1	286	1	GLAY_ECOLI1	TAGATOSE-BISPHOSPHATE	9	71e+01
166	6	1..1	286	1	GLAY_ECOLI1	TAGATOSE-BISPHOSPHATE	9	71e+01
167	6	1..1	290	1	GLAY_HNFV4	TAGATOSE-BISPHOSPHATE	9	71e+01
168	6	1..1	291	1	GLAY_HNFV4	TAGATOSE-BISPHOSPHATE	9	71e+01
169	6	1..1	292	1	CT1A_ECOLIA	CYTOSOLIC HSP70	9	71e+01
170	6	1..1	293	1	RS2_BAT	40S RIBOSOMAL PROTEIN	9	71e+01
171	6	1..1	293	1	RS2_HUMAN	40S RIBOSOMAL PROTEIN	9	71e+01
172	6	1..1	293	1	RS2_MOUSE	40S RIBOSOMAL PROTEIN	9	71e+01
173	6	1..1	293	1	RS2_MOUSE	40S RIBOSOMAL PROTEIN	9	71e+01
174	6	1..1	304	1	GLAY_HNFV5	TAGATOSE-BISPHOSPHATE	9	71e+01
175	6	1..1	306	1	CYSK_HELPY	CYSTEINE SYNTHASE (EC	9	71e+01
176	6	1..1	307	1	RM1_TIGR	HOMOBIOX PROTEIN HB1	9	71e+01
177	6	1..1	309	1	CT1_YEAST	CHAPERONIN 60	9	71e+01
178	6	1..1	309	1	CT1_YEAST	CHAPERONIN 60	9	71e+01
179	6	1..1	309	1	ER35_YEAST	GLYCOPOLYMERASE	9	71e+01
180	6	1..1	312	1	ER35_YEAST	GLYCOPOLYMERASE	9	71e+01
181	6	1..1	312	1	CCSA_ODJ51	OLFACTORY RECEPTOR-LIK	9	71e+01
182	6	1..1	316	1	GLA3_JACCE	BETA-LACTAMASE PRECURSOR	9	71e+01
183	6	1..1	316	1	GLA3_JACCE	BETA-LACTAMASE PRECURSOR	9	71e+01
184	6	1..1	323	1	FBUL_XENLA	FLUORIBILAN	9	71e+01
185	6	1..1	325	1	MCIR_SHEEP	MELANOCORTIN-5 RECEPTO	9	71e+01
186	6	1..1	325	1	MCIR_MOUSE	MELANOCORTIN-5 RECEPTO	9	71e+01
187	6	1..1	325	1	MCIR_MOUSE	MELANOCORTIN-5 RECEPTO	9	71e+01
188	6	1..1	325	1	MCIR_MOUSE	MELANOCORTIN-5 RECEPTO	9	71e+01
189	6	1..1	329	1	IG_GAMMA-3	IG GAMMA-3 CHAIN C REG	9	71e+01
190	6	1..1	329	1	ARAF_ECOLI1	L-ARABINOSE-BINDING PE	9	71e+01
191	6	1..1	330	1	GPB3_HUMAN	PROBABLE G PROTEIN-COU	9	71e+01
192	6	1..1	330	1	GPB3_HUMAN	PROBABLE G PROTEIN-COU	9	71e+01
193	6	1..1	330	1	TERP_YEAP	TERPENE SYNTHASE	9	71e+01
194	6	1..1	333	1	BC1X_HRCA	CHLOROPHYLLIDE REDUCTA	9	71e+01
195	6	1..1	333	1	DPD4_CARL	PUTATIVE PHOSPHATIDIS	9	71e+01
196	6	1..1	338	1	PLG_BACSU	FLAGELLAR MOTOR SWITCH	9	71e+01
197	6	1..1	340	1	SPG2_MOUSE	SPERMATOPHYTES SPAT	9	7

UD5-08-468-011a-2.rep

257	6	1, 1	438	1	HVCS, HETFR	IG HEAVY CHAIN C REGIO	9, 71e+01
258	6	1, 1	438	1	ALAU, MOUS	SERON ALBUMIN (FRAGEN)	9, 71e+01
259	6	1, 1	441	1	DIRR, ACHDO	DIURETIC (HORMONE) RECP	9, 71e+01
260	6	1, 1	441	1	DIRR, ACHDO	DIURETIC (HORMONE) RECP	9, 71e+01
261	6	1, 1	442	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
262	6	1, 1	442	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
263	6	1, 1	443	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
264	6	1, 1	443	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
265	6	1, 1	444	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
266	6	1, 1	445	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
267	6	1, 1	445	1	TBULIN, BETA CHAIN	TUBULIN BETA CHAIN	9, 71e+01
268	6	1, 1	452	1	CN17, DICDI	3, 5-CYCLOCYCLOPOTID	9, 71e+01
269	6	1, 1	452	1	PTCC, ECOLI	PTS SYSTEM, CELLOBIOSE	9, 71e+01
270	6	1, 1	454	1	PTCC, RHSDU	PTC PROTEIN	9, 71e+01
271	6	1, 1	454	1	PTCC, RHSDU	PTC PROTEIN	9, 71e+01
272	6	1, 1	457	1	IRB7, MOUSE	INTERFERON REGULATORY	9, 71e+01
273	6	1, 1	461	1	HVCS, HETFR	IG HEAVY CHAIN C REGIO	9, 71e+01
274	6	1, 1	461	1	NUAN, XENIA	NADH-UBIQUINONE OXIDOR	9, 71e+01
275	6	1, 1	461	1	NUAN, XENIA	NADH-UBIQUINONE OXIDOR	9, 71e+01
276	6	1, 1	465	1	CGRR, RAT	CALCIOTONIN GEM-RELATE	9, 71e+01
277	6	1, 1	465	1	CGRR, RAT	CALCIOTONIN GEM-RELATE	9, 71e+01
278	6	1, 1	467	1	ETUE, SALTY	6-PROSPIO BETA-GLUCOSI	9, 71e+01
279	6	1, 1	467	1	ETUE, SALTY	ETHANOLAMINE UTILITARI	9, 71e+01
280	6	1, 1	468	1	ETUE, SALTY	ETHANOLAMINE UTILITARI	9, 71e+01
281	6	1, 1	469	1	SEXY, YEAST	POTATIVE D-3-PROSPOOL	9, 71e+01
282	6	1, 1	469	1	SEXY, YEAST	POTATIVE D-3-PROSPOOL	9, 71e+01
283	6	1, 1	470	1	SHA, PIC	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
284	6	1, 1	470	1	SHA, PIC	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
285	6	1, 1	471	1	SHA, RAT	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
286	6	1, 1	471	1	SHA, RAT	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
287	6	1, 1	471	1	SHA, MOUSE	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
288	6	1, 1	471	1	IAAG, MAIZE	INDOLE-3-ACETATE BETA-	9, 71e+01
289	6	1, 1	471	1	SHA, HUMAN	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
290	6	1, 1	471	1	SHA, HUMAN	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
291	6	1, 1	471	1	SHA, CRGR	5-HYDROXYTRYPTAMINE 2A	9, 71e+01
292	6	1, 1	472	1	CB1R, HUMAN	CANNABINOID RECEPTOR 1	9, 71e+01
293	6	1, 1	473	1	CB1R, MOUSE	CANNABINOID RECEPTOR 1	9, 71e+01
294	6	1, 1	473	1	CB1R, MOUSE	C-2(428) STEROL REDUCT	9, 71e+01
295	6	1, 1	473	1	CB1R, MOUSE	C-2(428) STEROL REDUCT	9, 71e+01
296	6	1, 1	475	1	SEXY, MOUSE	PREPROTEIN TRANSLOCASE	9, 71e+01
297	6	1, 1	475	1	SEXY, MOUSE	PREPROTEIN TRANSLOCASE	9, 71e+01
298	6	1, 1	478	1	LVLD, PASSP	LEUCOKININ SECRETION P	9, 71e+01
299	6	1, 1	478	1	LVLD, PASSP	LEUCOKININ SECRETION P	9, 71e+01
300	6	1, 1	481	1	VLVD, JEMIN	GLUCOCORTICOID PUSYATE	9, 71e+01
301	6	1, 1	481	1	TRGN, TOBAC	PHOSPHOGLYCERATE KINAS	9, 71e+01
302	6	1, 1	483	1	TRGN, ECOLI	TRN SYSTEM POTASSIUM U	9, 71e+01
303	6	1, 1	484	1	PANF, HAZIN	SODIUM/PANICOTINATE ST	9, 71e+01
304	6	1, 1	484	1	PANF, HAZIN	SODIUM/PANICOTINATE ST	9, 71e+01
305	6	1, 1	487	1	YBDS, ECOLI	HYPOTHETICAL 53 K D P	9, 71e+01
306	6	1, 1	487	1	YBDS, ECOLI	HYPOTHETICAL 53 K D P	9

1	1	MODF_ECOLI	PUTATIVE MOYBIDIN-TR	9.71e+01
1	2	COXA1_PHYDE	CYTOCHROME C OXIDASE	9.71e+01
1	3	CPS3_P3	CYTOCHROME P450 XMIA3	9.71e+01
1	4	CPS3_P1G	CYTOCHROME P450 XMIA1	9.71e+01
1	5	CPS3_P1B	CYTOCHROME P450 XMIB	9.71e+01
1	6	CPS3_P1C	CYTOCHROME P450 XMIC	9.71e+01
1	7	CPS1_BOVIN	CYTOCHROME P450 XMIA1	9.71e+01
1	8	CALR_D1	CALCIUMION RECEPTOR PR	9.71e+01
1	9	YDR5_ECOLI	HYPOTHETICAL 54.0 KO P	9.71e+01
1	10	YDR5_ECOLI	HYPERBOLIC RECEPTOR	9.71e+01
1	11	YPS7_ECOLI	57 KDa PROTEIN	9.71e+01
1	12	G6P1_YTARO	GLUCOSE-6-PHOSPHATE IS	9.71e+01
1	13	CPY7_RAT	CYTOCHROME P450 XMIA1	9.71e+01
1	14	Y715_HUMAN	HYPOTHETICAL SODIUM-DE	9.71e+01
1	15	Y715_HUMAN	HYPERBOLIC RECEPTOR	9.71e+01
1	16	KIR1_HUMAN	SERINE/THREONINE-PROTE	9.71e+01
1	17	KIR4_MOUSE	SERINE/THREONINE-PROTE	9.71e+01
1	18	KASA_SHFL	AMINO ACID ANTIPORTER	9.71e+01
1	19	KASA_ECOLI	AMINO ACID ANTIPORTER	9.71e+01
1	20	KASA_ECOLI	AMINO ACID ANTIPORTER	9.71e+01
1	21	CATA_SUCPO	CEVASE (EC 1.11.1.6)	9.71e+01
1	22	TUP1_CANOE	TRANSCRIPTIONAL REPRES	9.71e+01
1	23	CAL1_MOUSE	CAUTIONION RECEPTOR PR	9.71e+01
1	24	CAL1_RAT	CAUTIONION RECEPTOR PR	9.71e+01
1	25	CAL1_RAT	CAUTIONION RECEPTOR PR	9.71e+01
1	26	NUC2_SINP7	NUB-PLASTOCYANONE OXI	9.71e+01
1	27	Y777_RATU	HYPOTHETICAL 56.3 KO P	9.71e+01
1	28	Y777_RATU	GLUCOSE TRANSPORTER TY	9.71e+01
1	29	PRO2_CANVO	DIETHYLMALIANE MONOX	9.71e+01
1	30	Y782_RATU	CAUTIONION RECEPTOR PR	9.71e+01
1	31	Y782_RATU	FUSION GLYCOPROTEIN P	9.71e+01
1	32	Y782_RATU	THIAMIN BIOSYNTHETIC B	9.71e+01
1	33	Y782_RATU	HISTIDYL-THIA SYNTHET	9.71e+01
1	34	FIB1_ADE40	FIBER PROTEIN	9.71e+01
1	35	FIB1_ADE40	FIBER PROTEIN	9.71e+01
1	36	FIB1_ADE40	60 KD INNER-MEMBRAN	9.71e+01
1	37	G01M_ECOLI	REGULATOR OF G-PROTEIN	9.71e+01
1	38	GLPD_BACSU	AEROBIC GLYCEROL-3-PHO	9.71e+01
1	39	EGLO_ECOLI	REGULATOR OF G-PROTEIN	9.71e+01
1	40	Y782_RATU	PYS SYSTEM, FRUCTOSE-5	9.71e+01
1	41	Y782_RATU	HYPERBOLIC PROTEIN H	9.71e+01
1	42	MERA_EKIN	MERCURIC REDUCTASE (EC	9.71e+01
1	43	MERA_EKIN	MERCURIC REDUCTASE (EC	9.71e+01
1	44	MERA_PSE41	MERCURIC REDUCTASE (EC	9.71e+01
1	45	FIB1_ADE41	FIBER PROTEIN 1	9.71e+01
1	46	Y782_RATU	CONVEX KINASE DBP20	9.71e+01
1	47	Y782_RATU	CELL CYCLE PROTEIN (K	9.71e+01
1	48	Y782_RATU	HYPOTHETICAL 64.6 KO P	9.71e+01
1	49	Y782_RATU	HYPOTHETICAL PROTEIN H	9.71e+01
1	50	Y782_RATU	HYPERBOLIC PROTEIN H	9.71e+01
1	51	DCPY_ASPOL	PHYTATE DECAHYDROXYLASE	9.71e+01
1	52	ASPA1_ECOLI	ARBENALIC PUMP-DRIVING	9.71e+01
1	53	ASPA1_ECOLI	ARBENALIC PUMP-DRIVING	9.71e+01

[illegible]

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I -> P (IN REF. 3).
E -> Q (IN REF. 3).
G -> A (IN REF. 3).
SEQUENCE 440 AA: 50206 MW: BCF5F5E4 CRC32:

Score 19: DB 1: Length 440;
Query Match 3.5%;
Best Local Similarity 100.0%; Pred. No. 5,52e-35;
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

167 PRRLKTEYIDHLEFVSP 185
169 PRRLKTEYIDHLEFVSP 187

RESULT 5
ID SCRC-RAT STANDARD: PRT: 449 AA.

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US-08-468-011A-2 RMD

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US-08-468-011A-2.rmp

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TRANSMEM 265      276      4 (POTENTIAL).
FF DOMAIN 277      296      EXTRACELLULAR (POTENTIAL).
FF TRANSMEM 297      308      CYTOPLASMIC (POTENTIAL).
FF FF TRANSMEM 309      317      5 (POTENTIAL).
FF DOMAIN 318      343      CYTOPLASMIC (POTENTIAL).
FF TRANSMEM 344      362      6 (POTENTIAL).
FF FF TRANSMEM 363      381      7 (POTENTIAL).
FF TRANSMEM 382      392      7 (POTENTIAL).
FF TRANSMEM 393      409      CYTOPLASMIC (POTENTIAL).
FF CARBOHYD 410      429      POTENTIAL.
FF FF TRANSMEM 430      449      POTENTIAL.
FF CARBOHYD 450      469      POTENTIAL.
FF FF TRANSMEM 470      489      POTENTIAL.
FF CARBOHYD 490      509      POTENTIAL.
FF FF SEQ SEQUENCE 449 AA: 51234 MP: 35394075 CRC12:

Query Match          3.5% Score: 19; DB 1; Length 449;
Best Local 19; Conservative 19; Identical 0; Gaps
Matches 0; Mismatches 0;

DB   167 PFRCTYNYHMLFVSP 185
    |||||
QY   169 PFRCTYNYHMLFVSP 187

RESULT 5
ID     PTRR_PIG 34, CREATED: PRT: 585 AA.
PS0133:
DT 01-OCT-1986 (REL. 34,
DE 01-NOV-1987 (REL. 35, LAST ANNOTATION UPDATE)
DD 01-NOV-1987 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DD PRECURSOR.
OS SUS SCROPA (P.).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTILA.
NC [ ] SEQUENCE FROM N.A.
NC MEDLINE: 96103158.
RA BLACK E.C.; SMITH D.P.; ZHANG X.Y.; FROLIK C.A., HARVEY A.,
RA CHANDRASEKHAR S., HEING H.M., 19-347(1986).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC RECEPTOR HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC SYSTEM AND cAMP/MAGNATIN/KINOSTOL-CALCIUM SECOND MESSENGER
CC SYSTEM. (B) SIMILARITY: INTEGRAL MEMBRANE PROTEIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC PROSITE: PS00164:G-PROTEIN_FPR_P3_1

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DR	PROSITE: P00650; G-PROTEIN COUPLED RECEPTOR: TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL	SEQ
FT	SIGNAL	1
FT	CHAIN	27
FT	DOMAIN	37
FT	DOMAIN	127
FT	DOMAIN	184
FT	DOMAIN	209
FT	TRANSMEM	216
FT	TRANSMEM	235
FT	DOMAIN	236
FT	TRANSMEM	278
FT	TRANSMEM	301
FT	DOMAIN	302
FT	TRANSMEM	312
FT	TRANSMEM	322
FT	DOMAIN	338
FT	TRANSMEM	357
FT	TRANSMEM	377
FT	DOMAIN	378
FT	TRANSMEM	405
FT	TRANSMEM	423
FT	TRANSMEM	436
FT	TRANSMEM	458
FT	DOMAIN	459
FT	CARBOHYD	147
FT	CARBOHYD	157
FT	CARBOHYD	167
FT	CARBOHYD	172
FT	CARBOHYD	173
FT	SEQUENCE	585 AA: 655682 NP_300438.6 CMC32:

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Query Match      33%  Score 18;  DB 1:331  Length 585;
Similarity 100%;  Positives 0;  Mismatches 0;  Indels 0;
Matches 18;  Conservative 0;
DBs
285 YPLATNYNVLVGLYLH 302
245 YPLATNYNVLVGLYLH 262
QY
RESULT 7
ID PTRR-MOUSE STANDARD; PRT: 591 AA.
AC PA1591; 062119;
DT 01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
GN PARHRN.
GN PTRR.
MUS MUSCULUS (MOUSE);
OC CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUMETAZOA; METAZOA;
OC EUTELENTEREA; ROENTHIA;
[1]
SEQUENCE FROM N.A.
AC KARPENIEN, VERNAN, DIJK T. B., HOSIOWAKERS T., CRECHES P.,
PC KARPENIEN, VERNAN, DIJK T. B., HOSIOWAKERS T., CRECHES P.,
RA ABOU-SAMRA A. S., BOONSTRA J., DE LAAT S.W., DEFFIJS L.H.K.;

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Query Match          3.3%   Score 18: DB 1: Length 591;
Best Local Similarity 100.0%; Pred. M. 1.1le-31;
Matches 18: Conservative O; Mismatches O; Indels O; G C

Db    290 YFATHTYTWLVEGLYLH 307
      |||||
QY    245 YFLATNTWLVESLYLH 262

RESULT 8
ID PTRL_RAT          STANDARD:          PRG: 591 AA.
AC P25961:            1992 (REL. 22, GENERATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE DE PRECURSOR.
OS RATIUS NORVICULUS (RAT).
OC EURAYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
NC 11
RC TISSUE=BONE.
RX MEDLINE: 92312903.
RA ABDO-SANRA A.-B., JUEPPNER R., FORCE T., FREEMAN M.W., KONG X.-F.
SA SCHNAPPA D., WERNER P.B., RICHARDS J., BONVETRE J.V., POTTS J.T.
EL PROC. NACL. ACAD. SCI. U.S.A. 89:2732-2736(1992).
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[2]	SEQUENCE FROM N.A.
RP	MEDLINE: 94392182
RX	PMID: 7651153
RY	JANIC N. N., RIVIERE M.,
RL	FUNCTIONS 20:20-36(1994).
RL	GENOMICS 20:20-36(1994).
CC	-1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC	PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC	CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSE
CC	NGER.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTO
DR	EMBL: M71848; G2060935; -
DR	GENBANK: U13716; 467317; -
DR	CDR3: L394732106
DR	PROSITE: PS00649; G-PROTEIN RECP_F2_1; 1.
DR	PROSITE: PS00650; G-PROTEIN RECP_F2_1; 1.
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT	SIGNAL 1 26 POTENTIAL.
FT	DOMAIN 1 26 POTENTIAL RECEPTOR.
FT	DOMAIN 27 188 EXTRACELLULAR POTENTIAL.

[illegible]

TRANSMEM	189	212	1 (POTENTIAL).
FT	190	213	2 (POTENTIAL).
FT	191	214	3 (POTENTIAL).
TRANSMEM	220	219	2 (POTENTIAL).
DONAN	240	282	EXTRACELLULAR (POTENTIAL).
TRANSMEM	283	306	3 (POTENTIAL).
FT	284	307	4 (POTENTIAL).
DONAN	307	370	CYTOPLASMIC (POTENTIAL).
TRANSMEM	310	371	5 (POTENTIAL).
FT	311	362	EXTRACELLULAR (POTENTIAL).
DONAN	343	361	6 (POTENTIAL).
TRANSMEM	362	382	5 (POTENTIAL).
FT	363	383	6 (POTENTIAL).
DONAN	383	409	CYTOPLASMIC (POTENTIAL).
TRANSMEM	410	478	7 (POTENTIAL).
FT	411	479	8 (POTENTIAL).
DONAN	440	460	9 (POTENTIAL).
TRANSMEM	441	463	7 (POTENTIAL).
FT	442	464	CYTOPLASMIC (POTENTIAL).
DONAN	464	591	POTENTIAL.
TRANSMEM	465	592	POTENTIAL.
FT	466	593	POTENTIAL.
CARBHYD	151	151	POTENTIAL.
FT	152	152	POTENTIAL.
CARBHYD	161	161	POTENTIAL.
FT	162	162	POTENTIAL.
CARBHYD	196	196	POTENTIAL.
FT	197	197	POTENTIAL.
CARBHYD	198	198	POTENTIAL.
FT	199	199	POTENTIAL.
SEQUENCE	591 AA:	66260 MW:	R5619777 CRC32:
5Q			

Query Match 3.3% Score 18; DB 1; Length 591;
Best Local Similarity 100.0% Pred No. 1, 11e-31;
Best Local Similarity 100.0% Pred No. 1, 11e-31;

	Matches	18;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
Dd	290	YFLATNYKWLVEGLYH	307						
Qv	245	YFLATNYKWLVEGLYH	262						

RESULT	9	
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DT	01-OCT-1993	(REL. 27, CREATED:
DT	01-OCT-1993	(REL. 27, LAST SOURCE UPDATE:
DT	01-SEP-1996	(REL. 31, LAST ACTION UPDATE:
DE	PARATHYROID HORMONE/	PARATHYROID HORMONE-RELATED
DE	PEPTIDE RECEPTOR	PRECUSOR.
DE	HOM SAPIENS (HUMAN).	
OC	EUARCTOTA: METAZOA:	CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC	EUMETAZOA: PRIMATES.	
OC	EUTHERIA: PRIMATES.	
OC	SEQUENCE FROM N.A.	
RC	TISSUE: KIDNEY.	
RC	MEDLINE: 93238641.	
EX	SCIPITANI E., KARGA H., KARAPIS A.C.	POOTS J.T. JR., KRONENBERG H.N.
RA	ENDOCRINOLOGY 132:2157-2165(1993).	
RA	SEQUENCE FROM N.A.	
RP	[2]	

MEDLINE: 91387403
 RX SCHNEIDER H., FEYEN J.-H., RAO MOYVA N.:
 RL EUR. J. PHARMACOL. 246:149-155(1993).
 RL [1]
 RL SOURCE FROM N.A.
 RX MEDLINE: 95263723
 RX SCHIPANI E., WEINSTEIN L.S., BERWITZ C., IIDA-KLEIN A., KONG X.F.,
 RL STURMAN M., KUSE K., WHITE M.P., MURRAY T., SCHMITZ J., DOP C.,
 RA ABUD-GAMBA A.B., SEGRE G.V., JEDERHARZ J.R., KROENBERG H.M.,
 RA J. CLIN. ENDOCRINOL. METAB. 80:1611-1621(1995).
 [4]
 RN SOURCE FROM N.A.
 RN RP TISSUE-KIDNEY
 RA LEVINE M.A.:
 RA
 CC SUBMITTED (XXI-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
 CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIN SECOND MESSENGER
 CC SYSTEM.
 CC -2- CELLULAR LOCATION: INTRACELL. MEMBRANE PROTEIN.
 CC -3- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
 CC KIDNEY, BONE AND LIVER.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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Tue Nov 24 08:11:00 1998

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AC	AC	01-NOV-1995 (REF. 32, LAST SEQUENCE UPDATE)		
DT	DT	01-NOV-1995 (REF. 32, LAST SEQUENCE UPDATE)		
DT	DT	01-NOV-1997 (REF. 35, LAST ANNOTATION UPDATE)		
DE	DE	GASTRO INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).		
DE	DE	DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR.		
OS	OS	RATTUS NORVEGICUS (RAT).		
OC	OC	EUMETAZOA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:		
OC	OC	EUTHERIA: RODENTIA.		
RP	RP	SEQUENCE FROM N.A.		
RC	RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN:		
RX	RX	MDLINE: 94062657.		
RA	RA	USDA 17-8, WEIZT E.; BUTTON D.C., BROWNSTEIN M.J., BONNER T.I.:		
CU	CU	FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS		
CC	CC	-11- FUNCTION: IS MEDIATED BY G PROTEINS WHICH ACTIVATES ADENYL		

Tue Nov 24 08:11:00 1998

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240 282 EXTRACELLULAR (POTENTIAL).
TRANSMEN 283 306
3 CYTOPLASMIC (POTENTIAL).
TRANSMEN 307 320
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TRANSMEN 321 342
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TRANSMEN 444 593
10 CYTOPLASMIC (POTENTIAL).
TRANSMEN 594 611
11 POTENTIAL.
TRANSMEN 612 661
12 POTENTIAL.
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TRANSMEN 677 691
14 K -> C (18 REF. 2).
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TRANSMEN 774 795
16 CONFLICT 473 473
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17 CONFLICT 473 473
TRANSMEN 831 845
18 CONFLICT 473 473
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133 CONFLICT 473 473
TRANSMEN 2571 2585
134 CONFLICT 473 473
TRANSMEN 2586 2600
135 CONFLICT 473 473
TRANSMEN 2601 2615
136 CONFLICT 473 473
TRANSMEN 2616 2630
137 CONFLICT 473 473
TRANSMEN 2631 2645
138 CONFLICT 473 473
TRANSMEN 2646 2660
139 CONFLICT 473 473
TRANSMEN 2661 2675
140 CONFLICT 473 473
TRANSMEN 2676 2690
141 CONFLICT 473 473
TRANSMEN 2691 2705
142 CONFLICT 473 473
TRANSMEN 2706 2720
143 CONFLICT 473 473
TRANSMEN 2721 2735
144 CONFLICT 473 473
TRANSMEN 2736 2750
145 CONFLICT 473 473
TRANSMEN 2751 2765
146 CONFLICT 473 473
TRANSMEN 2766 2780
147 CONFLICT 473 473
TRANSMEN 2781 2795
148 CONFLICT 473 473
TRANSMEN 2796 2810
149 CONFLICT 473 473
TRANSMEN 2811 2825
150 CONFLICT 473 473
TRANSMEN 2826 2840
151 CONFLICT 473 473
TRANSMEN 2841 2855
152 CONFLICT 473 473
TRANSMEN 2856 2870
153 CONFLICT 473 473
TRANSMEN 2871 2885
154 CONFLICT 473 473
TRANSMEN 2886 2900
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[illegible]

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Query Match          2.4%  Score 13: DB 1: Length 455;
Match Local Similarity 100.0%  Pred. No. 5.2e-16;
      13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      159 FRILCTRNYNHM 171
      |||||
.OY     169 FRILCTRNYNHM 181

RESULT 12
ID VIPR_HUMAN STANDARD: PRT: 457 AA.
AC P3224: Q15871:
DT 01-OCT-1993 (REL. 27, CREATED)
DE 1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DE 1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)

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FT CARBOHYD 292 292 POTENTIAL.
 50 SEQUENCE 455 AA: 52057 MW: 5642598 CRC32:
 Query Match 2.49; Score 13; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 5.28e-16;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 171 LKCTNINHLF 183
 Qy 172 LKCTNINHLF 184

RESULT 15
 ID GIPR_MESAO STANDARD; PRT: 462 AA.
 AC P43218;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
 DE MESOCICETUS AURATUS (GOLDEN HAMSTER).
 OS EUKARYOTA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RN [1] SEQUENCE FROM N.A.
 RA YASUDA K., INAGAKI N., YAMADA Y., KUBOTA A., SEINO S., SEINO Y.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1556-1562(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED INCLUDING PANCREATIC ISLET, STOMACH, BRAIN AND VARIOUS PERIPHERAL TISSUES.
 CC EMBL: D38103: G7855087; -1- BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR PROSITE: PS00649: G-PROTEIN_RECEP_F2_1: 1.
 DR PROSITE: PS00650: G-PROTEIN_RECEP_F2_2: 1.
 DR SIGNAL: 19 462 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT CHAIN 19 462
 FT DOMAIN 19 135
 FT TRANSHEM 136 158
 FT TRANSHEM 167 186
 FT TRANSHEM 187 214
 FT TRANSHEM 215 239
 FT TRANSHEM 240 264
 FT TRANSHEM 252 275
 FT TRANSHEM 276 290

RA YAMADA Y., IYAHARA T., NAKAMURA K., KASAKI P.J., SOMETA Y.,
 RA WANG C.E., SEINO S., SEINO Y.;
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED INCLUDING PANCREATIC ISLET, STOMACH, BRAIN AND VARIOUS PERIPHERAL TISSUES.
 CC EMBL: D38103: G7855087; -1- BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR PROSITE: PS00649: G-PROTEIN_RECEP_F2_1: 1.
 DR PROSITE: PS00650: G-PROTEIN_RECEP_F2_2: 1.
 DR SIGNAL: 19 462 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT CHAIN 19 462
 FT DOMAIN 19 135
 FT TRANSHEM 136 158
 FT TRANSHEM 167 186
 FT TRANSHEM 187 214
 FT TRANSHEM 215 239
 FT TRANSHEM 240 264
 FT TRANSHEM 252 275
 FT TRANSHEM 276 290

FT TRANSHEM 291 316
 FT DOMAIN 317 338
 FT TRANSHEM 339 359
 FT TRANSHEM 360 385
 FT TRANSHEM 396 462
 FT CARBOHYD 59 59
 FT TRANSHEM 60 60
 50 SEQUENCE 462 AA: 52918 MW: 4817702 CRC32:
 Query Match 2.49; Score 13; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 5.28e-16;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 159 PRLACTINYM 171
 Qy 169 PRLACTINYM 181

RESULT 16
 ID GIPR_MESAO STANDARD; PRT: 466 AA.
 AC P43218;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
 DE MESOCICETUS AURATUS (GOLDEN HAMSTER).
 OS EUKARYOTA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RN [1] SEQUENCE FROM N.A.
 RA USOLIN T.B., GRUBER C., MODI W., BONNER T.I.;
 RL SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED INCLUDING PANCREATIC ISLET, STOMACH, BRAIN AND VARIOUS PERIPHERAL TISSUES.
 CC EMBL: D38103: G7855087; -1- BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR PROSITE: PS00649: G-PROTEIN_RECEP_F2_1: 1.
 DR PROSITE: PS00650: G-PROTEIN_RECEP_F2_2: 1.
 DR SIGNAL: 19 462 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT CHAIN 19 462
 FT DOMAIN 19 135
 FT TRANSHEM 136 158
 FT TRANSHEM 167 186
 FT TRANSHEM 187 214
 FT TRANSHEM 215 239
 FT TRANSHEM 240 264
 FT TRANSHEM 252 275
 FT TRANSHEM 276 290

RA YAMADA Y., IYAHARA T., NAKAMURA K., KASAKI P.J., SOMETA Y.,
 RA WANG C.E., SEINO S., SEINO Y.;
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED INCLUDING PANCREATIC ISLET, STOMACH, BRAIN AND VARIOUS PERIPHERAL TISSUES.
 CC EMBL: D38103: G7855087; -1- BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 DR PROSITE: PS00649: G-PROTEIN_RECEP_F2_1: 1.
 DR PROSITE: PS00650: G-PROTEIN_RECEP_F2_2: 1.
 DR SIGNAL: 19 462 GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT CHAIN 19 462
 FT DOMAIN 19 135
 FT TRANSHEM 136 158
 FT TRANSHEM 167 186
 FT TRANSHEM 187 214
 FT TRANSHEM 215 239
 FT TRANSHEM 240 264
 FT TRANSHEM 252 275
 FT TRANSHEM 276 290

[3] SEQUENCE FROM N.A.
 RN TISSUE=PIUITARY;
 RX MEDLINE; 9335702;
 RA HARADA T., SHIGEMOTO R., MORI K., MACHIDA S.;
 RL NEURON 11:333-342(1993).
 [4]
 RN SEQUENCE FROM N.A.
 RN TISSUE=PIUITARY;
 RX MEDLINE; 93362505;
 RA SPENGLER D., WAEGER C., PANTALONI C., HOLSBOER P., BOCKHAERT J.,
 RA SEUBERG P.H., JOUROT L.;
 RL NATURE 365:170-175(1993).
 [5]
 RN SEQUENCE FROM N.A.
 RN TISSUE=OLFACTORY BULB;
 RX MEDLINE; 93359075;
 RA STRADINE-SPRAGUE-DAWLEY;
 RL NATURE 365:170-175(1993).
 [6]
 RN SEQUENCE OF 115-523 FROM N.A.
 RN STRAIN=WISTAR;
 RX MEDLINE; 93361875;
 RA COCARBELL R., RASTENWY M., CHRISTENSEN J.;
 RL SUBMITTED MAY 1993 TO ENGL/GENEANT/JOES DA NURS.
 [7]
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR PACAP-27 AND PACAP-38. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYL CYCLASE. THIS MAY REGULATE THE RELEASE OF ADRENOCORTICOTROPIN,
 CC GONADOTROPIN, AND PRL.
 CC CATECHOLAMINE. MAY PLAY A ROLE IN SPERMATOGENESIS AND SPERM
 CC MOTILITY. CAUSES SMOOTH MUSCLE RELAXATION AND SECRETION IN THE
 CC GASTROINTESTINAL TRACT.
 CC TISSUE SPECIFICITY: HYPOTHALAMIC, NEURAL, NEURONE PROTHIN.
 CC -1- TISSUE SPECIFICITY: HYPOTHALAMIC, ANTERIOR PITUITARY, ADRENAL
 CC MEDULLA, TESTICULAR GERM CELLS.
 CC -1- ALTERNATIVE PRODUCTS: FIVE DIFFERENT VARIANTS (HIP-HOP1, HOP1,
 CC HIP-HOP2 AND PACAP) CAN BE PRODUCED BY ALTERNATIVE SPLICING.
 CC THE SEQUENCE HEREIN IS THAT OF HIP-HOP1.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC ENBL; D16465; G457661; -
 CC ENBL; L16680; G347942; -
 CC ENBL; G14564; G457661; -
 CC ENBL; D14909; G457661; -
 CC ENBL; Z13721; G404196; -
 CC ENBL; Z13723; G404211; -
 CC ENBL; Z13725; G404228; -
 CC ENBL; Z13726; G404233; -
 CC ENBL; Z13719; G404353; -
 CC ENBL; Z13282; G397522; -
 CC ENBL; Z13282; G397521; -
 CC ENBL; Z13282; G397521; -
 CC ENBL; Z13735; G311329; -
 CC ENBL; Z13735; G311329; -

[illegible]

Dd		191 LFVFSMLRA 199	
Oy		183 LFVFSMLRA 191	
RESULT	29		
ID	P726_STYPL	STANDARD:	PRT: 117 AA.
AC	P38117	(REL. 24. CREATED)	
DT	01-DEC-1992	(REL. 24. LAST SEQUENCE UPDATE)	
DD	01-DEC-1992	(REL. 24. LAST ANNOTATION UPDATE)	
DE	PROTEIN-TYROSIENE PHOSPHATASE 25 (EC 3.1.3.48) (FRAGMENT).		
DG	ST 25 HILICATA (SEA SQUID).		
DN	EUKARYOTA; METAZOA; CHORDATA; TUNICATA.		
DR	[[]]		
DS	SEQUENCE FROM N.A.		
DT	MATHIAS R. FLORES E., THOMAS M.L.;		
DL	IMMUNOGNETHICS 33:33-41(1991).		
CC	N-1 CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H ₂ O =		
CC	ENL. PROTEIN TYROSINE + ORTHOPHOSPHATE.		
CG	PROSITE: P400191; TTL_PHOSPHATASE_1; PARTIAL.		
CN	PROSITE: PS0056; TTL_PHOSPHATASE_2; PARTIAL.		
CDR	PROSITE: PS0055; TTL_PHOSPHATASE_PTP_1.		
CE	NON-TER	1	
CF	NON-TER	1	
FT	NON-TER	117	
FQ	SEQUENCE	117 AA: 13422 MW; SEC(AA071) CKC32;	
		Query Match 1.5%; Score 8; DB 1; Length 117;	
		Best Local Similarity 100.0%; Pred. No. 1,05e+02;	
		Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dd	68 GSUJTVT 76		
Oy	449 GSUJTVI 456		
RESULT	30		
ID	VIPR_MELGA	STANDARD:	PRT: 260 AA.
AC	Q91085;		
DT	01-NOV-1997	(REL. 35. CREATED)	
DD	01-NOV-1997	(REL. 35. LAST SEQUENCE UPDATE)	
DE	01-NOV-1997	(REL. 35. LAST ANNOTATION UPDATE)	
DN	DE VASCOTACT INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR) (FRAGMENT).		
DR	GALLOPANO CONSON TURKEY.		
DS	EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOCHETALE;		
DT	KALLIPHORME.		
CC	EUKARYOTES		

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[1] SEQUENCE FROM N.A.
RP TISSUE-SMALL INTESTINE.
RC HSD C-C; YOU S.; EL HALAWANI M.E., FOSTER D.N.;
CA SUBMITTED JUN-1995 TO EMBL/GENBANK/DBJ DATA BANKS.
CC "1"-1: SUBCELLULAR LOCATION: CYTOSOL.
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE.
CC -1: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC PROSITE: P08064; G-PROTEIN RECEPTOR COUPLED RECEPTORS.
CC EMBL: U11981; G1289369; TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
DR PROSITE: P800649; G-PROTEIN RECEPT_F2_1; PARTIAL.
DR PROSITE: P800650; G-PROTEIN RECEPT_F2_2; 1.
FW SWISS-PROT: G-PROTEIN RECEPTOR; GLYCOPROTEIN.
SW DONAIDN <1 18 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 19 42 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 43 56 CYTOPLASMIC (POTENTIAL).
FT DONAIDN 57 95 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 96 119 5 (POTENTIAL).
FT DONAIDN 120 144 5 (POTENTIAL).
FT DONAIDN 145 176 6 (POTENTIAL).
FT TRANSMEM 177 196 7 (POTENTIAL).
FT DONAIDN 197 260 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 160 AA: 30358 MW: 82677GCP CRC32;
Query Match 1.5%; Score: 8; DB 1: Length 260;
Best Local Similarity 100.0%; Read No. 1:05e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
36 LVGLGYLTH 43
255 LVGLGYLTH 262
|||||||
DQ
QY
RESULT 31
ID YPEB_SVNP2 STANDARD; PRT: 411 AA.
AT P42784; 1995 (REL. 32, CREATED).
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DI 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE HYPOTHEETICAL PROTEIN IN PET5 5' REGION (FRAGMENT).
DS STREPTOCOCCUS SP. (STRAIN PCC 7002) (AGMELLIUM QUADRICAPITULUM).
OS STREPTOCOCCUS SP. (STRAIN PCC 7002) (AGMELLIUM QUADRICAPITULUM).
OC CYANOBACTERIA (BLUE-GREEN ALGAE); CHROMOCOCALLES.
[1]
RP SEQUENCE FROM N.A.
RC BIRCHWOOD 5194X.
CA BRAND S. N. TAN X. WIGDER W.R.

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CC      -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
OR      EMBL: U17858: G77455; -.
OR      EMBL: U17859: G77456; -.
OR      EMBL: U18936: C86764; -.
OR      PROSITE: P500649: G-PROTEIN RECP FL1: 1.
OR      PROSITE: P500650: G-PROTEIN RECP FL2: 1.
OR      PROSITE: P500651: G-PROTEIN RECP FL3: 1.
OR      SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS. TRANSDOMAINS: GLYCOPROTEIN; SIGNAL.
OR      SIGNAL: 1.
OR      CHAIN 25 431
OR      FT      DOMAIN 25 138
OR      FT      TRANSMEM 138 168
OR      FT      CYTOPLASMIC (POTENTIAL).
OR      FT      TRANSMEM 168 188
OR      FT      TRANSMEM 188 205
OR      FT      DOMAIN 189 205
OR      FT      DOMAIN 205 223
OR      FT      CYTOPLASMIC (POTENTIAL).
OR      FT      TRANSMEM 223 244
OR      FT      TRANSMEM 244 265
OR      FT      CYTOPLASMIC (POTENTIAL).
OR      FT      DOMAIN 266 284
OR      FT      TRANSMEM 285 307
OR      FT      TRANSMEM 307 325
OR      FT      CYTOPLASMIC (POTENTIAL).
OR      FT      TRANSMEM 325 350
OR      FT      TRANSMEM 351 365
OR      FT      CYTOPLASMIC (POTENTIAL).
OR      FT      TRANSMEM 366 385
OR      FT      TRANSMEM 385 408
OR      FT      CYTOPLASMIC (POTENTIAL).
OR      FT      CARBOHYD 408 411
OR      FT      CARBOHYD 411 421
OR      FT      CARBOHYD 421 431
OR      FT      CARBOHYD 431 441
OR      FT      CARBOHYD 441 451
OR      FT      CARBOHYD 451 461
OR      FT      CARBOHYD 461 471
OR      FT      CARBOHYD 471 481
OR      FT      CARBOHYD 481 491
OR      FT      CARBOHYD 491 500
OR      FT      CONFLICT 126 126
OR      FT      CONFLICT 392 393
OR      FT      CONFLICT 406 407
OR      FT      CONFLICT 408 408
OR      FT      CONFLICT 409 409
OR      FT      SEQUENCE 431 AA: 49923 MW: 4F433C7E C8E332;
Query Match 1.5%: Score 8; DB 1: Length 431;
Local Similarity 10%; Percent Identical 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
db 369 SFGQF535 376
db 1011111
db 403 SFGQF535 410
RESULT 38
SEQUENCE
P44958: Q13008; STANDARD;
AC 01-FEB-1994 (REL. 28; CREATED)
PRT: 444 AA.

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SEQ	CHAIN	25	444	
FF	TRANSHEN	25	121	1. (POTENTIAL).
FF	TRANSHEN	122	142	2. (POTENTIAL).
FF	TRANSHEN	143	163	3. (POTENTIAL).
FF	TRANSHEN	181	200	2. (POTENTIAL).
FF	TRANSHEN	201	218	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	219	242	3. (POTENTIAL).
FF	TRANSHEN	257	278	4. (POTENTIAL).
FF	TRANSHEN	259	278	5. (POTENTIAL).
FF	TRANSHEN	279	297	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	298	320	6. (POTENTIAL).
FF	TRANSHEN	321	343	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	344	363	7. (POTENTIAL).
FF	TRANSHEN	364	378	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	379	398	8. (POTENTIAL).
FF	TRANSHEN	399	414	9. (POTENTIAL).
FF	TRANSHEN	415	444	10. (POTENTIAL).
FF	CANBOHYD	45	45	POTENTIAL.
FF	CANBOHYD	78	78	POTENTIAL.
FF	CANBOHYD	90	90	POTENTIAL.
FF	CANBOHYD	100	100	POTENTIAL.
FF	CANBOHYD	116	116	POTENTIAL.
FF	VANSPLIC	41	81	MISSING (IN CRP-R3).
FF	VANSPLIC	146	174	GLUCANOLYTICWSPASQGLVPCAPFVQIRPHTN
FF	SEQUENCE	444 AA:	50719 MW: CABC3C3C CR3C3:	-> D (IN CRP-R3).
SSQ	SEQUENCE	444 AA:	50719 MW: CABC3C3C CR3C3:	MISSING (IN CRP-R2 AND CRP-R3).
Query Match		1.5%:	Score 8: DB 1: Length 444:	
Best Local Similarity		100.0%:	Pred. No: 1.05e-02:	
Matches		8: Conservative	0: Mismatches	0: Indels
db	382	SPOGFVFS 389		0: Gaps
db	403	SPOGFVFS 410		
FF	TRANSHEN	25	121	1. (POTENTIAL).
FF	TRANSHEN	122	142	2. (POTENTIAL).
FF	TRANSHEN	143	163	3. (POTENTIAL).
FF	TRANSHEN	181	200	2. (POTENTIAL).
FF	TRANSHEN	201	218	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	219	242	3. (POTENTIAL).
FF	TRANSHEN	257	278	4. (POTENTIAL).
FF	TRANSHEN	259	278	5. (POTENTIAL).
FF	TRANSHEN	279	297	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	298	320	6. (POTENTIAL).
FF	TRANSHEN	321	343	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	344	363	7. (POTENTIAL).
FF	TRANSHEN	364	378	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	379	398	8. (POTENTIAL).
FF	TRANSHEN	399	414	9. (POTENTIAL).
FF	TRANSHEN	415	444	10. (POTENTIAL).
FF	CANBOHYD	45	45	POTENTIAL.
FF	CANBOHYD	78	78	POTENTIAL.
FF	CANBOHYD	90	90	POTENTIAL.
FF	CANBOHYD	100	100	POTENTIAL.
FF	CANBOHYD	116	116	POTENTIAL.
FF	VANSPLIC	41	81	MISSING (IN CRP-R3).
FF	VANSPLIC	146	174	GLUCANOLYTICWSPASQGLVPCAPFVQIRPHTN
FF	SEQUENCE	444 AA:	50719 MW: CABC3C3C CR3C3:	-> D (IN CRP-R3).
SSQ	SEQUENCE	444 AA:	50719 MW: CABC3C3C CR3C3:	MISSING (IN CRP-R2 AND CRP-R3).
Query Match		1.5%:	Score 8: DB 1: Length 444:	
Best Local Similarity		100.0%:	Pred. No: 1.05e-02:	
Matches		8: Conservative	0: Mismatches	0: Indels
db	382	SPOGFVFS 389		0: Gaps
db	403	SPOGFVFS 410		
FF	TRANSHEN	25	121	1. (POTENTIAL).
FF	TRANSHEN	122	142	2. (POTENTIAL).
FF	TRANSHEN	143	163	3. (POTENTIAL).
FF	TRANSHEN	181	200	2. (POTENTIAL).
FF	TRANSHEN	201	218	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	219	242	3. (POTENTIAL).
FF	TRANSHEN	257	278	4. (POTENTIAL).
FF	TRANSHEN	259	278	5. (POTENTIAL).
FF	TRANSHEN	279	297	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	298	320	6. (POTENTIAL).
FF	TRANSHEN	321	343	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	344	363	7. (POTENTIAL).
FF	TRANSHEN	364	378	EXTRACELLULAR (POTENTIAL).
FF	TRANSHEN	379	398	8. (POTENTIAL).
FF	TRANSHEN	399	414	9. (POTENTIAL).
FF	TRANSHEN	415	444	10. (POTENTIAL).
FF	CANBOHYD	45	45	POTENTIAL.
FF	CANBOHYD	78	78	POTENTIAL.
FF	CANBOHYD	90	90	POTENTIAL.
FF	CANBOHYD	100	100	POTENTIAL.
FF	CANBOHYD	116	116	POTENTIAL.
FF	VANSPLIC	41	81	MISSING (IN CRP-R3).
FF	VANSPLIC	146	174	GLUCANOLYTICWSPASQGLVPCAPFVQIRPHTN

[illegible]

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Query Match      1.50; Score 8; DB 1; Length 533;
Best Local Similarity 100.00; Pred. No. 1.05e-02;
Matches      8; Conservative      0; Mismatches 0; Indels 0; Gaps 0;

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Db 133 LIPVAFFS 140
 Qy 264 LIPVAFFS 271

RESULTS 40
 ID 109R.BACSU STANDARD: PRT: 152 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-FEB-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-FEB-1987 (REL. 31, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
 RN
 RS
 RX SEQUENCE FROM N.A.
 RX MEDLINE: 86037230.
 RA BROIDA J., ABELSON J.:
 RL J. MOL. BIOL. 185:545-563(1985).
 RL J. MOL. BIOL. 185:545-563(1985).
 DR EMBL: J02516; G13864; AUT_INIT.
 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
 RN
 RS
 RX SEQUENCE FROM N.A.
 RX MEDLINE: 86037230.
 RA BROIDA J., ABELSON J.:
 RL J. MOL. BIOL. 185:545-563(1985).
 RL J. MOL. BIOL. 185:545-563(1985).
 DR EMBL: J02516; G13864; AUT_INIT.
 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
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 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
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 RL J. MOL. BIOL. 185:545-563(1985).
 DR EMBL: J02516; G13864; AUT_INIT.
 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
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 RX SEQUENCE FROM N.A.
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 DR EMBL: J02516; G13864; AUT_INIT.
 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
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 DR EMBL: J02516; G13864; AUT_INIT.
 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
 RN
 RS
 RX SEQUENCE FROM N.A.
 RX MEDLINE: 86037230.
 RA BROIDA J., ABELSON J.:
 RL J. MOL. BIOL. 185:545-563(1985).
 RL J. MOL. BIOL. 185:545-563(1985).
 DR EMBL: J02516; G13864; AUT_INIT.
 DR EMBL: J02516; G13864; AUT_INIT.
 PF: A04311; Z88P74.
 SQ SEQUENCE 152 AA; 1724 MW; 62B6692D CRC32;
 Query Match 1.3%; Score 7; DP 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.4e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 STIVLVL 86
 Qy 364 STIVLVL 370

RESULTS 41
 ID 109R.BACSU STANDARD: PRT: 178 AA.
 AC P54516;
 DT 01-OCT-1986 (REL. 34, CREAT. SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 GN 578 THE 37B PROTEIN (PROTEIN GP37B).
 GN 578 BACTERIOPHAGE T4.
 OC VIRIDAE: DS-DNA NONENVELOPED VIRUSES: MYOVIRIDAE.
 RN
 RS
 RX SEQUENCE FROM N.A.
 RX MEDLINE: 86037230.
 RA BROIDA J., ABELSON J.:
 RL J. MOL. BIOL. 185:545-563(198

```

P47992;
AC   01-FEB-1996 (REL. 33, CREATED)
DT   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DI   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DR   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
GN   R131.3: CERNOMORPHIN PROTEIN L6.
GC   CAENORRABDITIS ELIGANS.
OC   EUMETAZOA: METAZOA: ACCELONATES: NEMATODA; SECERNENTEA; RHABDITIDA.
CC   FURTHER INFORMATION:
SC   SEQUENCE FROM N.A.
RA   STRAIN-BRISTOL M2;
RC   FULTON L.;
RL   SUBMITTED (FEB-1984), TO ENBL/GENBANK/DDJ DATA BANKS.
RG   SUBMITTED (MAY-1996), TO THE LAB FAMILY OF RIBOSOMAL PROTEINS.
DC   EMBL D84432; G456927.
GG   EMBL D84432; G456927.
DR   WORMPEP; R151.3; CER0744.
DR   PROSITE; PS01170; RIBOSOMAL_L6E: 1.
KW   RIBOSOMAL PROTEIN.
SQ   SEQUENCE 217 AA; 24313 MW; AIA6293D CRC32;

Query Match          1.3% Score 7; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Db      181 APTLAAI 187
QY      |||||
        320 APTLAAI 326

RESULT  44
ID   YQLBACSU STANDARD; PRT: 253 AA.
AC   P54549: 1986 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DI   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DR   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GN   YQLBACSU.
GC   HYPOCHLORELLA SP. 2.2 KD PROTEIN IN GLN4-ANSR INTERGENIC REGION.
OC   FUCHSIACEAE.
CC   YEAST-LIKE SUPRILLES.
SC   SEQUENCE 253 AA; 28172 MW; 7D3D6178 CRC32;
RA   PRKARYOTIA; FRIMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
[1]
RP   SEQUENCE FROM N.A.
RG   STRAIN-169 / JH642;
DR   SUBMITTED (MAY-1996), TO ENBL/GENBANK/DDJ DATA BANKS.
CC   SATO T; TAKECHI M.; MASUDA S., TAKEHARU K., HOSHINO S.,
RA   SUBMITTED (MAY-1996), TO ENBL/GENBANK/DDJ DATA BANKS.
DI   D84432; G1303963;
DR   EMBL D84432; G1303963;
GC   HYPOCHLORELLA SP. 2.2 KD PROTEIN IN GLN4-ANSR INTERGENIC REGION.
KW   HYPOCHLORELLA.
SQ   SEQUENCE 253 AA; 28172 MW; 7D3D6178 CRC32;
```

```

Query Match      1.38; Score 7; DB 1; Length 268;
Best Local Similarity 100.0%;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Db      14 LSCSLA 20
Ty      16 LSCSLA 22

```

[illegible][illegible]

Tue Nov 24 08:11:00 1998

A. ROSEN H., DOUGLASS J., WEINERT E.
 J. BIOL. CHEM. 259, 14109-14111 (1984).
 (5)
 SEQUENCE FROM N.A.
 TISSUE: HEART; 7256
 C. C. 100
 BAO S.M., ROWLETS R.D.,
 REGUL. PEPT. 40:197-408 (1992).
 C. C. 100
 !- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART AND TESTIS.
 C. C. 100
 !- FTYR: THE INTERNAL CONTAINS 6 CONSERVED CYSTINES THOUGHT TO
 BE INVOLVED IN THE FORMATION OF A DISULFIDE-BINDING
 !- SIMILARITY: BELONGS TO THE OPIOIDS NEUROPEPTIDES PRECURSORS
 FAMILY.
 EMBL: 549481; G359153; -
 C. C. 100
 C. C. 100
 EMBL: 507503; G56130; -
 C. C. 100
 PIR: A01475; Q0174.
 C. C. 100
 PIR: A05081; A05081.
 C. C. 100
 PIR: S03892; S03892.
 C. C. 100
 PROSITE: P01251; OPIOIDS PRECURSOR. 1.
 C. C. 100
 CLEAVAGE OR PAIR OF BASIC RESIDUES: SIGNAL; ENDORPHIN; NEUROPEPTIDE.
 OPIOID PEPTIDE.
 SIGNAL 100 24
 MET-ENKEPHALIN 1.
 T. T. PEPTIDE 107 111
 MET-ENKEPHALIN 2.
 T. T. PEPTIDE 136 140
 MET-ENKEPHALIN 3.
 T. T. PEPTIDE 189 195
 MET-ENKEPHALIN-ARG-GLY-LEU.
 T. T. PEPTIDE 212 216
 LEU-ENKEPHALIN 4.
 T. T. PEPTIDE 261 269
 LEU-ENKEPHALIN-ARG-PHE.
 T. T. CONFLICT -12 12
 L -> V (IN REF. 3 AND 4).

```

Query Match      1.3%; Score 7; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.41e+00;
Matches          0; Mismatches 0; Indels 0; Gaps 0;
Conservative     7;

```

D	YDIA_ECOLI	STANDARD:	PRT: 277 AA.
C	P03822	P46137; P76203;	
T	21-JUL-1986 (REL. 01, CREATED)		
T	31-OCT-1997 (REL. 35, LAST SEQUENCE UPDATE)		
T	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
N	HYPOTHETICAL 31.2 KD PROTEIN IN PPSA-AROM INTERGENIC REGION.		
N	YDIA.		

Query Match 1.39; Score 7; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Nov 24 08:11:00 1998

US-08-468-011A-2.rpd

PEPTIDE	136	140	MET-ENKEPHALIN 3.
PEPTIDE	188	195	MET-ENKEPHALIN-ARG-SER-LEU.
PEPTIDE	212	216	MET-ENKEPHALIN 4.
PEPTIDE	218	222	MET-ENKEPHALIN 5.
PEPTIDE	263	269	MET-ENKEPHALIN-ARG-PHE.
CONFLICT	34	34	T -> S (IN REF 2).
CONFLICT	184	184	MISSING (IN REF 2).
SEQUENCE	269 AA:	31105 MB:	7D0895B3;RCJ32:

```

Query Match      1.38: Score 7: DB 1: Length 269:
Best Local Similarity 100.0%: Pred. No. 1.41e+00:
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

9      14 LGSCLLA 20
      |||||
16 LGSCLLA 22

```

RESULT 47
PENK BAT STANDARD; PRF; 269 AA.
040594;
01-NOV-1986 (REL. 03, CREATED)
01-NOV-1986 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROKEPHALIN A PRECURSOR.
PENK.
RATTUS NORVIGICUS (RAT).
CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
(1)
SEQUENCE FROM N.A.
TISSUE-BRAIN;
HOWELLS R.D. 6950.
DOWENHILL R.D. 6950.
HOFERFRIEND S.;
PROC. NATL. ACAD. SCI. U.S.A. 81:7651-7655(1984).
(1)
SEQUENCE FROM N.A.
TISSUE-BRAIN;
MEDLINE: 85054887.
YOSHIMAWA K., WIGGANS C., SAROL S.L.;
37 EMB. CHIM. 255:14301-14306(1984).
(4)
SEQUENCE FROM N.A.
STRAIN=MISTAR; TISSUE=TESTIS;
YOSHIMAWA K., MARGUTTA K., AZAWA T., YANAMOTO A.;
FEBS LETT. 246:193-196(1989).
(4)
SEQUENCE FROM N.A.
STRAIN=MISTAR; TISSUE=TESTIS;
MEDLINE: 85054887.

Tue Nov 24 08:11:00 1998

UIC-08-468-0113-3-100

[illegible]

Query Match 1.39; Score 7; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.41e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

.....
MUSENLAH (TM)
.....
Release J.A. John F. Collins, Bloomsbury Research Unit.
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Distribution rights by Oxford Molecular Ltd
MParch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Nov 23 13:38:43 1998; MacPar time 20.58 seconds
Tabular output not generated.
Title: >US-08-468-011A-2
Description: (1-541) from US08468011A.pap
Sequence: 1 MAWGLSHVWMLGSL.....DDLMEKSPRNENPDTGG 541
Scoring table: TABLE unitprotobase
Searched: 120441 seqs, 36531193 residues
Post-processing: Minimum Match 04
Listing first 100 summaries
Database: plr56
Statistics: Mean 3.707; Variance 0.454; scale 8.168
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Match Length DB ID Description Pred. No.
.....
1 413 76.3 550 2 A57519 parathyroid hormone r 0.00e+00

53 7 1.3 253 2 D69964 conserved hypothetical 4.36e+00
54 7 1.3 268 2 I53029 preproenkephalin A - 4.36e+00
55 7 1.3 269 2 B55678 enkephalin precursor 4.36e+00
56 7 1.3 270 2 B55678 enkephalin precursor 4.36e+00
57 7 1.3 271 2 Q68244 hypothetical vda pro 4.36e+00
58 7 1.3 289 2 A34783 myogenesis protein Ny 4.36e+00
59 7 1.3 324 2 S05396 hypothetical protein 4.36e+00
60 7 1.3 325 2 S05396 hypothetical protein 4.36e+00
61 7 1.3 340 2 S05396 quinine oxidoreductase 4.36e+00
62 7 1.3 360 2 B55082 ysg2 protein - Bacher 4.36e+00
63 7 1.3 360 2 A43255 membrane-bound hydrolase 4.36e+00
64 7 1.3 363 1 H02008 hydroxylase (EC 1.1.18) 4.36e+00
65 7 1.3 378 2 S05092 SGT1 protein 4.36e+00
66 7 1.3 378 2 S05092 SGT1 protein 4.36e+00
67 7 1.3 401 2 B37416 bloodstream-specific 4.36e+00
68 7 1.3 422 2 D69958 conserved hypothetical 4.36e+00
69 7 1.3 461 3 J00097 secreted 45K protein 4.36e+00
70 7 1.3 461 3 J00097 secreted 45K protein 4.36e+00
71 7 1.3 472 2 B76262 hypothetical protein 4.36e+00
72 7 1.3 553 2 B46222 osmoprotection protein 4.36e+00
73 7 1.3 544 1 R28544 mercuroyl(II) reductase 4.36e+00
74 7 1.3 544 2 S74503 hypothetical protein 4.36e+00
75 7 1.3 544 2 S74503 hypothetical protein 4.36e+00
76 7 1.3 602 2 A45769 acetylcholine receptor 4.36e+00
77 7 1.3 739 2 J00581 vascular cell adhesion 4.36e+00
78 7 1.3 826 2 I38372 hypothetical protein 4.36e+00
79 7 1.3 826 2 I38372 hypothetical protein 4.36e+00
80 7 1.3 1189 2 B44117 hypothetical protein 4.36e+00
81 7 1.3 1203 2 S05094 chromosomal protein X 4.36e+00
82 7 1.3 1339 2 S20052 DNA-directed DNA poly 4.36e+00
83 7 1.3 3005 2 S31642 hemostatic protein rfb- 4.36e+00
84 6 1.1 37 2 S05094 hypothetical protein 4.36e+00
85 6 1.1 37 2 S05094 hypothetical protein 4.36e+00
86 6 1.1 30 2 A36733 hypothetical protein 1.98e+02
87 6 1.1 30 2 S0347 4-hydroxybenzoyl-CoA 1.98e+02
88 6 1.1 37 2 E70005 hypothetical protein 1.98e+02
89 6 1.1 37 2 E70005 hypothetical protein 1.98e+02
90 6 1.1 75 2 S05094 ribosomal protein L14 1.98e+02
91 6 1.1 85 2 S75163 hypothetical protein 1.98e+02
92 6 1.1 87 2 A69341 cobalt transport prot 1.98e+02
93 6 1.1 88 2 S05139 R+-transporting ATP as 1.98e+02
94 6 1.1 88 2 S05139 R+-transporting ATP as 1.98e+02
95 6 1.1 92 2 D64901 hypothetical protein 1.98e+02
96 6 1.1 94 2 S44064 antifungal protein pr 1.98e+02
97 6 1.1 96 2 D69769 hypothetical protein 1.98e+02
98 6 1.1 101 2 B46598 ekt-related protein S 1.98e+02
99 6 1.1 101 2 B46598 ekt-related protein S 1.98e+02
100 6 1.1 104 2 A22706 vitelline membrane pr 1.98e+02
101 6 1.1 108 2 J01428 hypothetical 11.6K pr 1.98e+02
102 6 1.1 113 2 F63441 hypothetical protein 1.98e+02
103 6 1.1 114 2 F48564 hypothetical protein 1.98e+02

acidic elicitor A1 - 1.98e+02
hypothetical protein 1.98e+02
humoral defense prote 1.98e+02
hypothetical protein 1.98e+02
hypothetical protein 1.98e+02
probable lipoprotein 1.98e+02
perB protein - Bacher 1.98e+02
mRNA suppressor prote 1.98e+02
ribosomal protein S9 1.98e+02
hypothetical protein 1.98e+02
nodulin-5 precursor - 1.98e+02
hypothetical protein 1.98e+02
hemoglobin alpha chai 1.98e+02
hemoglobin alpha chai 1.98e+02
hemoglobin alpha chai 1.98e+02
M protein P6M49 - St 1.98e+02
hypothetical protein 1.98e+02
hypothetical protein 1.98e+02
hypothetical protein 1.98e+02
hemoglobin alpha chai 1.98e+02
8-oxo-7,8-dihydrogua 1.98e+02
furcose-6-phosphate m 1.98e+02
reductase, assembly p 1.98e+02
major pollen allergen 1.98e+02
NADH dehydrogenase (u 1.98e+02
NADH dehydrogenase (u 1.98e+02
DNA-type molecular c 1.98e+02
hypothetical protein 1.98e+02
ATPase subunit 6 (ATP 1.98e+02
hypothetical protein 1.98e+02
hypothetical protein 1.98e+02
pancreatic lipase-asac 1.98e+02
hypothetical protein 1.98e+02
hypothetical protein 1.98e+02
fibriol protein 987P 1.98e+02
ribosomal protein S7 1.98e+02
ribosomal protein S7, 1.98e+02
cutinase (EC 3.1.1.3) 1.98e+02
cutinase (EC 3.1.1.3) 1.98e+02
hypothetical 21.5K pr 1.98e+02

155	6	1.1	197	2	526493	translation initiation	1.99e+02
156	6	1.1	201	2	A64203	hypothetical protein	1.99e+02
157	6	1.1	202	2	B62110	conserved hypothetical	1.99e+02
158	6	1.1	203	2	D885C	conserved hypothetical	1.99e+02
159	6	1.1	204	2	B62110	succinate dehydrogenase	1.99e+02
160	6	1.1	205	2	B31906	hypothetical protein	1.99e+02
161	6	1.1	207	2	A53895	nitrophorin 1 precursor	1.99e+02
162	6	1.1	208	2	B62110	hypothetical protein	1.99e+02
163	6	1.1	210	2	B32977	hypothetical protein	1.99e+02
164	6	1.1	211	2	B45444	hypothetical protein	1.99e+02
165	6	1.1	211	2	B66091	divC 5'-region hypot	1.99e+02
166	6	1.1	218	2	B64338	conserved hypothetical	1.99e+02
167	6	1.1	219	2	B64338	conserved hypothetical	1.99e+02
168	6	1.1	219	2	ORC9C	glutamine transporter	1.99e+02
169	6	1.1	219	2	B47082	dnaK-type molecular c	1.99e+02
170	6	1.1	221	2	B02156	NADH dehydrogenase (u	1.99e+02
171	6	1.1	221	2	A41333	glycerol metabolism a	1.99e+02
172	6	1.1	221	2	B64338	hypothetical protein	1.99e+02
173	6	1.1	221	2	A31139	ribosomal protein S2	1.99e+02
174	6	1.1	221	2	B02828	floral homeotic prote	1.99e+02
175	6	1.1	224	2	B32728	hypothetical protein	1.99e+02
176	6	1.1	224	2	B01862	hypothetical protein	1.99e+02
177	6	1.1	224	2	B64338	glutathione peroxidase	1.99e+02
178	6	1.1	225	2	C45550	R+-transporting ATP a	1.99e+02
179	6	1.1	226	2	B26156	R+-transporting ATP a	1.99e+02
180	6	1.1	226	2	PM06C	cap-binding protein p	1.99e+02
181	6	1.1	226	2	B64338	hypothetical protein	1.99e+02
182	6	1.1	226	2	B41895	H+-transporting ATP a	1.99e+02
183	6	1.1	226	2	B64338	H+-transporting ATP a	1.99e+02
184	6	1.1	226	2	B64338	H+-transporting ATP a	1.99e+02
185	6	1.1	227	2	PM06C	hypothetical protein	1.99e+02
186	6	1.1	227	2	PM06C	cap-binding protein p	1.99e+02
187	6	1.1	230	2	B64338	conserved hypothetical	1.99e+02
188	6	1.1	233	2	B51383	ig lambda chain - an	1.99e+02
189	6	1.1	234	2	B08652	dnaK-type molecular c	1.99e+02
190	6	1.1	235	2	B32728	ribosomal protein S2	1.99e+02
191	6	1.1	235	2	B32728	ribosomal protein S2	1.99e+02
192	6	1.1	241	2	B65332	glucose-1-phosphate c	1.99e+02
193	6	1.1	242	2	A45724	pectate lyase (EC 4.2	1.99e+02
194	6	1.1	242	2	B71757	MADS box protein DEFR	1.99e+02
195	6	1.1	243	2	B65332	hypothetical 26.3 kD	1.99e+02
196	6	1.1	243	2	B65332	hypothetical 26.3 kD	1.99e+02
197	6	1.1	246	2	B01472	tryptophan (EC 3.4.21.4)	1.99e+02
198	6	1.1	246	2	B01472	tryptophan (EC 3.4.21.4)	1.99e+02
199	6	1.1	247	2	B41819	serotonin 2 receptor	1.99e+02
200	6	1.1	248	2	B64338	hypothetical protein	1.99e+02
201	6	1.1	248	2	B64338	hypothetical protein	1.99e+02
202	6	1.1	255	2	D70146	hypothetical protein	1.99e+02
203	6	1.1	255	2	B72067	u0002m protein - Myco	1.99e+02
204	6	1.1	255	2	B72067	hypothetical protein	1.99e+02
205	6	1.1	280	2	C61139	biotin synthesis prot	1.99e+02

206	6	1.1	261	2	J01024	hypothetical 30K prot	1.99e+02
207	6	1.1	261	2	A36098	lactose phosphotransf	1.99e+02
208	6	1.1	262	2	B69665	required for formate	1.99e+02
209	6	1.1	262	2	B69665	hypothetical protein	1.99e+02
210	6	1.1	262	2	B69665	hypothetical protein	1.99e+02
211	6	1.1	266	2	B31863	1'-acyl-sn-glycerol-3-	1.99e+02
212	6	1.1	269	2	D46668	hypothetical protein	1.99e+02
213	6	1.1	270	2	J04350	thioesteron - strept	1.99e+02
214	6	1.1	270	2	B64338	ureid protein	1.99e+02
215	6	1.1	270	2	B32977	chitinase (EC 3.2.1.1	1.99e+02
216	6	1.1	270	2	B32977	chitinase (EC 3.2.1.1	1.99e+02
217	6	1.1	271	2	B50207	hypothetical protein	1.99e+02
218	6	1.1	271	2	B50207	hypothetical protein	1.99e+02
219	6	1.1	277	2	B64338	hypothetical protein	1.99e+02
220	6	1.1	278	2	B64338	hypothetical protein	1.99e+02
221	6	1.1	284	2	A40590	lateral flagellin - v	1.99e+02
222	6	1.1	284	2	B69232	inosine-5'-monophosph	1.99e+02
223	6	1.1	284	2	B69232	inosine-5'-monophosph	1.99e+02
224	6	1.1	285	2	B69232	inosine-5'-monophosph	1.99e+02
225	6	1.1	285	2	B69232	inosine-5'-monophosph	1.99e+02
226	6	1.1	285	2	B69232	inosine-5'-monophosph	1.99e+02
227	6	1.1	286	2	B69232	inosine-5'-monophosph	1.99e+02
228	6	1.1	286	2	B69232	inosine-5'-monophosph	1.99e+02
229	6	1.1	286	2	B69232	inosine-5'-monophosph	1.99e+02
230	6	1.1	292	2	B72323	ubiquinol-cytochrome	1.99e+02
231	6	1.1	292	2	C65070	hypothetical protein	1.99e+02
232	6	1.1	293	2	B32728	ribosomal protein S2	1.99e+02
233	6	1.1	294	2	B72323	hypothetical protein	1.99e+02
234	6	1.1	294	2	B72323	hypothetical protein	1.99e+02
235	6	1.1	295	2	B64818	hypothetical 31.3 kD	1.99e+02
236	6	1.1	295	2	B64818	hypothetical 31.3 kD	1.99e+02
237	6	1.1	301	2	B40201	hypothetical protein	1.99e+02
238	6	1.1	301	2	B40201	hypothetical protein	1.99e+02
239	6	1.1	306	2	C45333	cysteine synthetase -	1.99e+02
240	6	1.1	307	2	B04923	homeotic protein Hox	1.99e+02
241	6	1.1	309	2	C65338	ubiquinol-cytochrome	1.99e+02
242	6	1.1	309	2	C65338	ubiquinol-cytochrome	1.99e+02
243	6	1.1	309	2	C65338	ubiquinol-cytochrome	1.99e+02
244	6	1.1	312	2	B72323	cytochrome c-type syn	1.99e+02
245	6	1.1	316	2	B65332	beta-lactamase (EC 3.	1.99e+02
246	6	1.1	316	2	B65332	beta-lactamase (EC 3.	1.99e+02
247	6	1.1	316	2	B65332	beta-lactamase (EC 3.	1.99e+02
248	6	1.1	323	2	B31417	serine hydroxymethylt	1.99e+02
249	6	1.1	325	2	B72323	hypothetical protein	1.99e+02
250	6	1.1	325	2	B72323	hypothetical protein	1.99e+02
251	6	1.1	325	2	B72323	hypothetical protein	1.99e+02
252	6	1.1	325	2	B72323	hypothetical protein	1.99e+02
253	6	1.1	329	2	J062A	melanocyte-stimulat	1.99e+02
254	6	1.1	329	2	B46678	endoglycosidase F3 (E	1.99e+02
255	6	1.1	329	2	B46678	endoglycosidase F3 (E	1.99e+02
256	6	1.1	330	2	B46678	endoglycosidase F3 (E	1.99e+02

257	6	1.1	330	2	A55689	G-protein-coupled rec	1.99e+02
258	6	1.1	333	2	B17823	proteochlorophyllide r	1.99e+02
259	6	1.1	333	2	B49850	chlorin reductase sub	1.99e+02
260	6	1.1	335	2	C27895	hypothetical protein	1.99e+02
261	6	1.1	337	2	B31863	hypothetical protein	1.99e+02
262	6	1.1	337	2	B31863	hypothetical protein	1.99e+02
263	6	1.1	338	2	B43368	flagellar motor switc	1.99e+02
264	6	1.1	340	2	B60601	photorepair protein p	1.99e+02
265	6	1.1	340	2	B60601	photorepair protein p	1.99e+02
266	6	1.1	340	2	B60601	photorepair protein p	1.99e+02
267	6	1.1	342	2	C47084	spore photoproduct ly	1.99e+02
268	6	1.1	344	2	GRV67C	sulfate transport pro	1.99e+02
269	6	1.1	344	2	B52264	probable galactosyltr	1.99e+02
270	6	1.1	344	2	B52264	probable galactosyltr	1.99e+02
271	6	1.1	347	2	ORC9C	crithine carbamoylir	1.99e+02
272	6	1.1	350	2	B75065	sensory transduction	1.99e+02
273	6	1.1	350	2	B49531	Enn protein - strepto	1.99e+02
274	6	1.1	350	2	B49531	hypothetical protein	1.99e+02
275	6	1.1	350	2	B49531	hypothetical protein	1.99e+02
276	6	1.1	351	2	B66620	rod outer segment mem	1.99e+02
277	6	1.1	351	2	B66620	rod outer segment mem	1.99e+02
278	6	1.1	352	2	B69743	hypothetical protein	1.99e+02
279	6	1.1	352	2	B69743	hypothetical protein	1.99e+02
280	6	1.1	353	2	A43667	proteic kinase h rel	1.99e+02
281	6	1.1	354	2	B75877	hypothetical protein	1.99e+02
282	6	1.1	354	2	B64475	GRP-binding protein,	1.99e+02
283	6	1.1	356	2	A43350	phosphate transport p	1.99e+02
284	6	1.1	356	2	A43350	phosphate transport p	1.99e+02
285	6	1.1	358	2	B70185	27 protein - human pa	1.99e+02
286	6	1.1	360	2	C70185	carotenoid biosynthes	1.99e+02
287	6	1.1	361	2	B57895	hypothetical protein	1.99e+02
288	6	1.1	361	2	B57895	hypothetical protein	1.99e+02
289	6	1.1	361	2	B57895	phosphate transfer pr	1.99e+02
290	6	1.1	362	2	B57895	phosphate transfer pr	1.99e+02
291	6	1.1	362	2	B57895	phosphate transfer pr	1.99e+02
292	6	1.1	362	2	B57895	phosphate transfer pr	1.99e+02
293	6	1.1	364	2	B61346	cell division protein	1.99e+02
294	6	1.1	364	2	B61346	cell division protein	1.99e+02
295	6	1.1	366	2	A46604	MHC PD14 transplanat	1.99e+02
296	6	1.1	366	2	A46604	MHC PD14 transplanat	1.99e+02
297	6	1.1	366	2	A46604	MHC PD14 transplanat	1.99e+02
298	6	1.1	366	2	A46604	MHC PD14 transplanat	1.99e+02
299	6	1.1	367	2	B39649	lipoprotein - Actinob	1.99e+02
300	6	1.1	368	2	C69984	conserved hypothetical	1.99e+02
301	6	1.1	372	2	B49008	melanocortin-5 recept	1.99e+02
302	6	1.1	372	2	B49008	melanocortin-5 recept	1.99e+02
303	6	1.1	376	2	B31740	hypothetical protein	1.99e+02
304	6	1.1	376	2	B31740	hypothetical protein	1.99e+02
305	6	1.1	377	2	B50147	alcohol dehydrogenase	1.99e+02
306	6	1.1	377	2	B50147	alcohol dehydrogenase	1.99e+02
307	6	1.1	377	2	B50147	beta-hydroxysteroid	1.99e+02
308	6	1.1	380	2	B50147	beta-hydroxysteroid	1.99e+02
309	6	1.1	380	2	B50147	GTP-binding regulator	1.99e+02

308	6	1.1	381	2	A59689	response regulator as	1.99e+02
309	6	1.1	382	2	B39780	subtilisin (EC 3.4.21	1.99e+02
310	6	1					

359	6	1,1	445	A44949	tubulin beta chain -	1.98e+02
360	6	1,1	445	J00120	tubulin beta chain -	1.98e+02
361	6	1,1	445	U820P	tubulin beta chain -	1.98e+02
362	6	1,1	449	S2016	purine permease homol	1.98e+02
363	6	1,1	449	S2016	tubulin beta chain -	1.98e+02
364	6	1,1	449	S16340	tubulin beta chain -	1.98e+02
365	6	1,1	450	S40383	outer membrane protei	1.98e+02
366	6	1,1	451	S76671	hypothetical protein	1.98e+02
367	6	1,1	452	S76671	hypothetical protein	1.98e+02
368	6	1,1	452	A23546	3',5'-cyclic-nucleoti	1.98e+02
369	6	1,1	455	S2	albumin homology - hum	1.98e+02
370	6	1,1	461	QX147	MDH dehydrogenase (u	1.98e+02
371	6	1,1	461	QX147	MDH dehydrogenase (u	1.98e+02
372	6	1,1	461	S2	calcitonin receptor-1	1.98e+02
373	6	1,1	464	S20592	hypothetical protein	1.98e+02
374	6	1,1	464	S16034	calcitonin-like recep	1.98e+02
375	6	1,1	465	S2	phosphatase-11, autoi	1.98e+02
376	6	1,1	465	S65020	phosphatase-11, autoi	1.98e+02
377	6	1,1	469	S48370	probable phosphoglyce	1.98e+02
378	6	1,1	469	S2	probable phosphoglyce	1.98e+02
379	6	1,1	471	S40689	5-hydroxytryptamine 2	1.98e+02
380	6	1,1	471	S40689	5-hydroxytryptamine 2	1.98e+02
381	6	1,1	471	A54739	indole 3-acetate beta	1.98e+02
382	6	1,1	471	S11280	serotonin receptor 5H	1.98e+02
383	6	1,1	471	A34863	serotonin receptor 5H	1.98e+02
384	6	1,1	472	S2	GTP-binding regulator	1.98e+02
385	6	1,1	472	S2	cannabinoid receptor	1.98e+02
386	6	1,1	473	S33117	sugar transporter pr	1.98e+02
387	6	1,1	473	S69789	probable transporter pr	1.98e+02
388	6	1,1	473	S40141	probable transporter pr	1.98e+02
389	6	1,1	475	S40141	probable transporter pr	1.98e+02
390	6	1,1	475	H64318	preprotein transloase	1.98e+02
391	6	1,1	475	S15337	heat shock protein Ht	1.98e+02
392	6	1,1	477	S49937	SOK outer membrane pr	1.98e+02
393	6	1,1	477	S49937	SOK outer membrane pr	1.98e+02
394	6	1,1	478	D30160	calcitonin receptor	1.98e+02
395	6	1,1	479	S33746	calcitonin receptor c	1.98e+02
396	6	1,1	479	S59652	lincomycin-resistance	1.98e+02
397	6	1,1	479	A11368	keratin type II, hair	1.98e+02
398	6	1,1	479	A11368	keratin type II, hair	1.98e+02
399	6	1,1	482	A39285	calcitonin receptor-1	1.98e+02
400	6	1,1	483	S2	hypothetical protein	1.98e+02
401	6	1,1	484	S64105	pyrophosphate transp	1.98e+02
402	6	1,1	487	S24785	cytochrome P450 - mou	1.98e+02
403	6	1,1	487	S24785	cytochrome P450 - mou	1.98e+02
404	6	1,1	487	S64795	hypothetical protein	1.98e+02
405	6	1,1	489	S276768	hypothetical protein	1.98e+02
406	6	1,1	490	S2	probable molybdenum t	1.98e+02
407	6	1,1	490	S2	probable molybdenum t	1.98e+02
408	6	1,1	490	S2	cytochrome P45011C -	1.98e+02
409	6	1,1	492	S432525	steroid 21 monooxygen	1.98e+02

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512	6	1	1	713	2	5X013D	phosphotransacetylase	1	1996-02
513	6	1	1	714	2	G50357	phosphate acetyltrans	1	1996-02
514	6	1	1	714	2	G65001	phosphate acetyltrans	1	1996-02
515	6	1	1	714	2	A06014	penicillin-binding pr	1	1996-02
516	6	1	1	714	2	A06014	penicillin-binding pr	1	1996-02
517	6	1	1	730	2	A51064	folded gastrulation c	1	1996-02
518	6	1	1	749	2	A37839	expopolysaccharonat	1	1996-02
519	6	1	1	766	2	G37684	hypochelatal protein	1	1996-02
520	6	1	1	766	2	G37684	hypochelatal protein	1	1996-02
521	6	1	1	772	1	VP0883	outer layer protein v	1	1996-02
522	6	1	1	776	1	VP0883	outer layer protein v	1	1996-02
523	6	1	1	776	1	G24410	hypochelatal protein	1	1996-02
524	6	1	1	783	2	G02755	outer membrane prot	1	1996-02
525	6	1	1	783	2	G02755	outer membrane prot	1	1996-02
526	6	1	1	809	2	G55344	cadherin 11 - huma	1	1996-02
527	6	1	1	809	2	G55344	outer envelope membra	1	1996-02
528	6	1	1	815	2	G55344	outer envelope membra	1	1996-02
529	6	1	1	815	2	G55344	outer envelope membra	1	1996-02
530	6	1	1	844	2	G21667	mannosyltransferase (1	1996-02
531	6	1	1	852	1	JV0821V	DNA mismatch repair p	1	1996-02
532	6	1	1	859	2	QJ2267	DNA packaging protei	1	1996-02
533	6	1	1	860	2	QJ2267	lipoygenase (EC 1.1.3	1	1996-02
534	6	1	1	860	2	QJ2267	lipoygenase (EC 1.1.3	1	1996-02
535	6	1	1	885	2	S30350	beta-alpha-tyrosin 1	1	1996-02
536	6	1	1	886	2	A37558	intra-amyloid like pro	1	1996-02
537	6	1	1	886	2	G54355	inter-alpha-inhibitor	1	1996-02
538	6	1	1	889	2	G54355	inter-alpha-inhibitor	1	1996-02
539	6	1	1	889	2	G54355	inter-alpha-tyrosin 1	1	1996-02
540	6	1	1	908	1	QJ1938	structural core prote	1	1996-02
541	6	1	1	908	2	JN0804	nitrate reductase (NA	1	1996-02
542	6	1	1	911	2	G70901	transferrin-binding p	1	1996-02
543	6	1	1	911	2	G70901	transferrin-binding p	1	1996-02
544	6	1	1	912	2	G64107	transferrin-binding p	1	1996-02
545	6	1	1	914	2	G70906	transferrin-binding p	1	1996-02
546	6	1	1	916	2	A34418	jockey protein 2 - fr	1	1996-02
547	6	1	1	916	2	A34418	jockey protein 2 - fr	1	1996-02
548	6	1	1	942	2	QJ1674	protein kinase - yeast	1	1996-02
549	6	1	1	942	2	G53963	protein kinase - yeast	1	1996-02
550	6	1	1	945	2	S30398	aminopeptidase N homo	1	1996-02
551	6	1	1	977	1	QJ1531	glutamy aminopeptid	1	1996-02
552	6	1	1	977	1	QJ1531	glutamy aminopeptid	1	1996-02
553	6	1	1	982	2	A52523	thermoactive cellulase	1	1996-02
554	6	1	1	986	2	G12021	thermoactive cellulase	1	1996-02
555	6	1	1	994	2	I43276	c-met tyrosine kinase	1	1996-02
556	6	1	1	994	2	I43276	c-met tyrosine kinase	1	1996-02
557	6	1	1	1004	2	G23231	major outer surface glycop	1	1996-02
558	6	1	1	1005	1	PIV067	RNA 1 protein - psau	1	1996-02
559	6	1	1	1007	2	A30093	beta-galactosidase (E	1	1996-02
560	6	1	1	1009	2	G602148	protein-tyrosine kinase	1	1996-02
561	6	1	1	1009	2	G602148	protein-tyrosine kinase	1	1996-02
562	6	1	1	1009	2	G032330	cell adhesion kinase 2	1	1996-02

767	5	0.9	5249238	gamma	4.11e+03
768	5	0.9	5249396	modi-hemolysin gamma	4.11e+03
769	5	0.9	5249496	modi-hemolysin - Brady	4.11e+03
770	5	0.9	700441	oligopeptide ABC tran	4.11e+03
771	5	0.9	5249597	hypothetical protein	4.11e+03
772	5	0.9	5249697	hypothetical protein	4.11e+03
773	5	0.9	344082	branched-chain-amino-	4.11e+03
774	5	0.9	309	glutamine homolog y	4.11e+03
775	5	0.9	309823	glutamine homolog y	4.11e+03
776	5	0.9	5249797	NS-methyltetrahydrom	4.11e+03
777	5	0.9	5249897	hypothetical protein	4.11e+03
778	5	0.9	5249997	hypothetical protein	4.11e+03
779	5	0.9	5250097	hypothetical protein	4.11e+03
780	5	0.9	5250197	hypothetical protein	4.11e+03
781	5	0.9	5250297	hypothetical protein	4.11e+03
782	5	0.9	5250397	hypothetical protein	4.11e+03
783	5	0.9	5250497	hypothetical protein	4.11e+03
784	5	0.9	5250597	hypothetical protein	4.11e+03
785	5	0.9	5250697	hypothetical protein	4.11e+03
786	5	0.9	5250797	hypothetical protein	4.11e+03
787	5	0.9	5250897	hypothetical protein	4.11e+03
788	5	0.9	5250997	hypothetical protein	4.11e+03
789	5	0.9	5251097	hypothetical protein	4.11e+03
790	5	0.9	5251197	hypothetical protein	4.11e+03
791	5	0.9	5251297	hypothetical protein	4.11e+03
792	5	0.9	5251397	hypothetical protein	4.11e+03
793	5	0.9	5251497	hypothetical protein	4.11e+03
794	5	0.9	5251597	hypothetical protein	4.11e+03
795	5	0.9	5251697	hypothetical protein	4.11e+03
796	5	0.9	5251797	hypothetical protein	4.11e+03
797	5	0.9	5251897	hypothetical protein	4.11e+03
798	5	0.9	5251997	hypothetical protein	4.11e+03
799	5	0.9	5252097	hypothetical protein	4.11e+03
800	5	0.9	5252197	hypothetical protein	4.11e+03
801	5	0.9	5252297	hypothetical protein	4.11e+03
802	5	0.9	5252397	hypothetical protein	4.11e+03
803	5	0.9	5252497	hypothetical protein	4.11e+03
804	5	0.9	5252597	hypothetical protein	4.11e+03
805	5	0.9	5252697	hypothetical protein	4.11e+03
806	5	0.9	5252797	hypothetical protein	4.11e+03
807	5	0.9	5252897	hypothetical protein	4.11e+03
808	5	0.9	5252997	hypothetical protein	4.11e+03
809	5	0.9	5253097	hypothetical protein	4.11e+03
810	5	0.9	5253197	hypothetical protein	4.11e+03
811	5	0.9	5253297	hypothetical protein	4.11e+03
812	5	0.9	5253397	hypothetical protein	4.11e+03
813	5	0.9	5253497	hypothetical protein	4.11e+03
814	5	0.9	5253597	hypothetical protein	4.11e+03
815	5	0.9	5253697	hypothetical protein	4.11e+03
816	5	0.9	5253797	hypothetical protein	4.11e+03
817	5	0.9	5253897	hypothetical protein	4.11e+03

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869	5	0.9	S19723	hydrolytic protease	4.1e+03	
870	5	0.9	S02068	RNA-directed RNA poly	4.1e+03	
871	5	0.9	4710	hypothetical protein	4.1e+03	
872	5	0.9	4711	6-phosphofructo-2-kin	4.1e+03	
873	5	0.9	4712	serine/threonine-spec	4.1e+03	
874	5	0.9	4713	asparagine-tRNA ligase	4.1e+03	
875	5	0.9	4714	alpha-amylase (EC 3.2	4.1e+03	
876	5	0.9	S23257	hypothetical protein	4.1e+03	
877	5	0.9	4772	pyruvate assimilation	4.1e+03	
878	5	0.9	4773	pyruvate assimilation	4.1e+03	
879	5	0.9	S40887	aldehyde dehydrogenase	4.1e+03	
880	5	0.9	S12266	aldehyde dehydrogenase	4.1e+03	
881	5	0.9	4871	DDBP18	actin homolog	4.1e+03
882	5	0.9	4872	S47508	actin homolog	4.1e+03
883	5	0.9	4873	S47509	actin homolog	4.1e+03
884	5	0.9	4955	S10651	glycine G1 precursor	4.1e+03
885	5	0.9	4956	A49930	casein protein homolog	4.1e+03
886	5	0.9	A40555	envelope protein - Ja	4.1e+03	
887	5	0.9	A40556	envelope protein - Ja	4.1e+03	
888	5	0.9	WPK47	serine/threonine-spec	4.1e+03	
889	5	0.9	S145009	serine/threonine-spec	4.1e+03	
890	5	0.9	S123202	probable aspartate tr	4.1e+03	
891	5	0.9	S123203	probable aspartate tr	4.1e+03	
892	5	0.9	S123204	probable aspartate tr	4.1e+03	
893	5	0.9	S123205	probable aspartate tr	4.1e+03	
894	5	0.9	WJ2931	cellulose 1,4-beta-gl	4.1e+03	
895	5	0.9	A23931	glucosylceramidase (E	4.1e+03	
896	5	0.9	S17451	halohydrin R4 (EC 3.4	4.1e+03	
897	5	0.9	S2320	halohydrin R4 (EC 3.4	4.1e+03	
898	5	0.9	PN0108	halohydrin R4 (EC 3.4	4.1e+03	
899	5	0.9	S412	signal recognition pa	4.1e+03	
900	5	0.9	S413	signal recognition pa	4.1e+03	
901	5	0.9	S414	nif-specific regulato	4.1e+03	
902	5	0.9	S31949	thiolglutathione (EC 3	4.1e+03	
903	5	0.9	S415	thiolglutathione (EC 3	4.1e+03	
904	5	0.9	S61297	heat-shock protein or	4.1e+03	
905	5	0.9	S61298	heat-shock protein or	4.1e+03	
906	5	0.9	S64537	L-lactate permease -	4.1e+03	
907	5	0.9	S522	succinate dehydrogen	4.1e+03	
908	5	0.9	S69464	succinate dehydrogen	4.1e+03	
909	5	0.9	S69465	succinate dehydrogen	4.1e+03	
910	5	0.9	HMV168	phosphatase	4.1e+03	
911	5	0.9	HMV169	phosphatase	4.1e+03	
912	5	0.9	HMV170	phosphatase	4.1e+03	
913	5	0.9	S44186	malate synthase (EC 4	4.1e+03	
914	5	0.9	S44187	malate synthase (EC 4	4.1e+03	
915	5	0.9	S44188	malate synthase (EC 4	4.1e+03	
916	5	0.9	S69880	major structural nucl	4.1e+03	
917	5	0.9	S69881	major structural nucl	4.1e+03	
918	5	0.9	S69882	hypothetical protein	4.1e+03	
919	5	0.9	S69883	hypothetical protein	4.1e+03	
920	5	0.9	S69884	hypothetical protein	4.1e+03	
921	5	0.9	S69885	hypothetical protein	4.1e+03	
922	5	0.9	S69886	hypothetical protein	4.1e+03	
923	5	0.9	S69887	hypothetical protein	4.1e+03	
924	5	0.9	S69888	hypothetical protein	4.1e+03	
925	5	0.9	S69889	hypothetical protein	4.1e+03	
926	5	0.9	S69890	hypothetical protein	4.1e+03	
927	5	0.9	S69891	hypothetical protein	4.1e+03	
928	5	0.9	S69892	hypothetical protein	4.1e+03	
929	5	0.9	S69893	hypothetical protein	4.1e+03	
930	5	0.9	S69894	hypothetical protein	4.1e+03	
931	5	0.9	S69895	hypothetical protein	4.1e+03	
932	5	0.9	S69896	hypothetical protein	4.1e+03	
933	5	0.9	S69897	hypothetical protein	4.1e+03	
934	5	0.9	S69898	hypothetical protein	4.1e+03	
935	5	0.9	S69899	hypothetical protein	4.1e+03	
936	5	0.9	S69900	hypothetical protein	4.1e+03	

920	5	0.9	WADP dehydrogenase (u	4.1e+03
921	5	0.9	transcriptional initiat	4.1e+03
922	5	0.9	actin-binding protein	4.1e+03
923	5	0.9	probable membrane pro	4.1e+03
924	5	0.9	beta-2-microglobulin	4.1e+03
925	5	0.9	actin-gelatinase [c	4.1e+03
926	5	0.9	AEC transporter (ATP-	4.1e+03
927	5	0.9	EL protein - human pa	4.1e+03
928	5	0.9	gp70 protein - murine	4.1e+03
929	5	0.9	phosphatidylesterase	4.1e+03
930	5	0.9	nucleoside transport	4.1e+03
931	5	0.9	levanase sacC - Bacil	4.1e+03
932	5	0.9	transketolase (EC 2.2	4.1e+03
933	5	0.9	hypothetical protein	4.1e+03
934	5	0.9	hypothetical protein	4.1e+03
935	5	0.9	hypothetical protein	4.1e+03
936	5	0.9	bone morphogenetic pr	4.1e+03
937	5	0.9	meprin A (EC 3. 24.1	4.1e+03
938	5	0.9	RNA-directed RNA pol	4.1e+03
939	5	0.9	RNA-directed RNA pol	4.1e+03
940	5	0.9	anhydrilase synthase	4.1e+03
941	5	0.9	RNA-directed RNA pol	4.1e+03
942	5	0.9	hypothetical protein	4.1e+03
943	5	0.9	hypothetical protein	4.1e+03
944	5	0.9	pyocin AP41 large cha	4.1e+03
945	5	0.9	chemotaxis protein fr	4.1e+03
946	5	0.9	conserved hypothetical	4.1e+03
947	5	0.9	nerve growth factor	4.1e+03
948	5	0.9	nerve growth factor	4.1e+03
949	5	0.9	DNA topoisomerase (EC	4.1e+03
950	5	0.9	fibronectin gamma 1 ac	4.1e+03
951	5	0.9	fibronectin gamma 1 ac	4.1e+03
952	5	0.9	translation elongatio	4.1e+03
953	5	0.9	vesiculan - pig tailed	4.1e+03
954	5	0.9	methionine synthase m	4.1e+03
955	5	0.9	phosphomethylpruvate c	4.1e+03
956	5	0.9	phosphomethylpruvate c	4.1e+03
957	5	0.9	protein-tyrosine kin	4.1e+03
958	5	0.9	neurofilament triplet	4.1e+03
959	5	0.9	lipoxysynthase 1-2 tr	4.1e+03
960	5	0.9	phosphatase 1-2 tr	4.1e+03
961	5	0.9	phA002C protein - Myc	4.1e+03
962	5	0.9	poly(epsilon)-lysine p	4.1e+03
963	5	0.9	poly(epsilon)-lysine p	4.1e+03
964	5	0.9	dicar-large tumor sup	4.1e+03
965	5	0.9	kinase heavy chain	4.1e+03
966	5	0.9	translation elongatio	4.1e+03
967	5	0.9	kinaseC1-associate pe	4.1e+03
968	5	0.9	atrial neurotrophic pe	4.1e+03
969	5	0.9	atrial neurotrophic pe	4.1e+03
970	5	0.9	atrial neurotrophic pe	4.1e+03
971	5	0.9	atrial neurotrophic pe	4.1e+03
972	5	0.9	atrial neurotrophic pe	4.1e+03
973	5	0.9	atrial neurotrophic pe	4.1e+03
974	5	0.9	atrial neurotrophic pe	4.1e+03
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985	5	0.9	atrial neurotrophic pe	4.1e+03
986	5	0.9	atrial neurotrophic pe	4.1e+03
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1000	5	0.9	atrial neurotrophic pe	4.1e+03

971	5	9	1122	2	52437	protein-tyrosine kinase	41e-03
972	5	9	1133	2	150297	pytochrome A, potato	41e-03
973	5	9	1134	1	A35955	meta-vinculin, human	41e-03
974	5	9	1135	1	A29927	meta-vinculin, chick	41e-03
975	5	9	1136	1	A29927	meta-vinculin, human	41e-03
976	5	9	1207	2	C70013	conserved hypothetical	41e-03
977	5	9	1218	2	Q50069	hypothetical 110X pro	41e-03
978	5	9	1250	1	TVZRWU	protein-tyrosine kinase	41e-03
979	5	9	1261	1	527224	N-methyl-D-aspartate	41e-03
980	5	9	1275	2	527224	N-methyl-D-aspartate	41e-03
981	5	9	1358	2	643436	Phosphoribosylformyl	41e-03
982	5	9	1392	1	TVBYAD	L-aminoadipate-semal	41e-03
983	5	9	1400	2	138195	protein-tyrosine kinase	41e-03
984	5	9	1401	2	138195	protein-tyrosine kinase	41e-03
985	5	9	1704	2	A55426	phosphoglucomutase	41e-03
986	5	9	1763	1	RHMWF9	RNA-directed RNA poly	41e-03
987	5	9	1786	1	RHMWF9	RNA-directed RNA poly	41e-03
988	5	9	1786	1	RHMWF9	RNA-directed RNA poly	41e-03
989	5	9	1805	2	W05521	laminin chain B1 prec	41e-03
990	5	9	1850	2	C12332	ubiquitin-protein 1	41e-03
991	5	9	1885	2	S12151	hypothetical protein	41e-03
992	5	9	2105	1	A44059	RNA-directed RNA poly	41e-03
993	5	9	2105	1	A44059	probable RNA-directed	41e-03
994	5	9	2284	1	C65070	RNA-directed RNA poly	41e-03
995	5	9	2317	2	156752	c-ras-1 tyrosine kinase	41e-03
996	5	9	2338	2	173957	c-ras-1 tyrosine kinase	41e-03
997	5	9	2481	2	A43908	fibronectin, African	41e-03
998	5	9	2503	2	A43908	fibronectin, African	41e-03
999	5	9	2663	2	955505	fat-sodium acceptor	41e-03
1000	5	9	5032	2	A35041	ryanodine receptor type	41e-03

	ALIGNMENTS
RESULT	A57519
SEQUENCE	stype complex
DESCRIPTION	parathyroid hormone receptor 2 precursor - human
FEATURES	PtI2 receptor
ALTERNATE_NAMES	afmr1; gene homo sapiens common_name man
ORGANISM	Homo sapiens
DATE	sequence_revision 00-Dec-1995 start_change 03-Aug-1997
ACCESSIONS	A35519
REFERENCES	Dobryzcka, T.B.; Guber, C.; Bonner, T.J.
AUTHORS	Dobryzcka, T.B.
JOURNAL	J. Biol. Chem. (1995) 270:15455-15458
TITLE	Identification and functional expression of a receptor recognizing parathyroid hormone the PtI2 receptor

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#accession      A57519
#status         Preliminary; nucleic acid sequence not shown
#molecule_type mRNA

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119-08-468-011A-3 452

virginiana common_name North American opossum
24-Jan-1992 sequence_revision 24-Jan-1992 text_change
A3286
A3286

author Juppner, R.; Abou-Saure, A.B.; Freeman, M.; Kong, X.F.;
Porte JT., Jr.; Kronenberg, H.M.; Sagre, G.V.

science (1991) 254:1024-1026

A O protein-linked receptor for parathyroid hormone and
parathyroid-related peptide.

cross-references NIDB:92054592

eccection A3286

primary: non-compared with conceptual translation
#molecule_type RNA
#residues 468
#cross-referenced DB:M74445
#comment: ligand: parathyroid hormone related protein.
length 595 aminoacids; weight 68007; cenehmus B339

Query Match 4.6%; Score 25; DB 2; length 595;
Local Similarity 10.6%; Pos 468; Neg 468;
Matches 25; Conservative

207 GFFRRRLACTNYINDHFLVPSMURA 131
167 GFPRALACTNYINDHFLVPSMURA 121

[illegible]

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06 NOV 24 09:11:00 1998      US-08-468-011A-2.TPR

SUMMARY          length 440   emolecular-weight 50234   checksum 7684

Query Match      3.5%: Score 19; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 3 64e+30;
Matches 19; Conservative 0; Alimatches 0; Indels 0; Gaps 0;

Db 167 FRRLCTNTYIHMLFVSF 185
QY 169 FRRLCTNTYIHMLFVSF 187

RESULT 4
AUTHOR           SUGIJO         type complete
TITLE            secretin receptor
ORGANISM          Rattus norvegicus
DATE             13-Jan-1995 sequence_revision 13-Jan-1995 #text_Change
ACCESSIONS       S16319
REFERENCE        Ishihara, T.; Nakamura, S.; Kasiro, Y.; Takahashi, T.;
                  Takahashi, K.; Nagata, S.
                  Molecular cloning and expression of a cDNA encoding the
                  secretin receptor.
                  J Biol Chem 269:11045-11051
EMOLCULE_TYPE    SUGIJO     preliminary
across-references MIMD:91266890
KEYWORDS          secretin receptor; secretin; parathyroid hormone related peptide
SUMMARY          length 449   emolecular-weight 51234   checksum 33

Query Match      3.5%: Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1 64e+30;
Matches 19; Conservative 0; Alimatches 0; Indels 0; Gaps 0;

Db 167 FRRLCTNTYIHMLFVSF 185
QY 169 FRRLCTNTYIHMLFVSF 187

RESULT 5
AUTHOR           IS9297        type complete
TITLE            parathyroid hormone-related peptide
                  receptor - mouse
ORGANISM          Mus musculus
DATE             28-Feb-1997 sequence_revision 03-Jul-1996 #text_Change
ACCESSIONS       I59297
REFERENCE        I59297
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280-312 domain transmembrane status predicted label TM\N
 313-354 domain transmembrane status predicted label TM\N
 355-396 domain transmembrane status predicted label TM\N
 400-431 domain transmembrane status predicted label TM\N
 432-431 domain transmembrane status predicted label TM\N
 93.104.135.328 binding site carbohydrate (Aa) (covalent) status predicted
 111 binding site phosphate (Thr) (covalent) (by protein kinase A) status predicted
 285 binding site phosphate (Ser) (covalent) (by protein kinase A) status predicted
 485 binding site phosphate (Ser) (covalent) (by protein kinase A) status predicted
 SUMMARY length 492 molecular-weight 55591 checksum 1077

Query Match
 Best Local Similarity 100.04; Pred. No. 1.17e-13;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 205 LINCNTNRYH 217
 QY 177 LINCNTNRYH 184

RESULT 14
 ENTRY title
 ALTERNATE_NAMES
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCES
 #authors
 #submission
 #accession
 #molecule_type mRNA
 #residues 1-466 #label BON
 #cross-references EMBL:U39231; NID:G1066050; PID:G1066051

GENETICS
 #name GDB:GIPR
 #cross-references GDB:335023
 #map_position 19q13.3-19q13.3
 #length 466 molecular-weight 53156 checksum 265

Summary
 Query Match
 Best Local Similarity 100.04; Pred. No. 4.08e-11;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 162 FRLNCTNRYH 173
 QY 169 FRLNCTNRYH 180

QY 169 FRLNCTNRYH 180

RESULT 15
 ENTRY title
 ALTERNATE_NAMES
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCES
 #authors
 #journal
 #title
 #accession
 #status preliminary
 #molecule_type mRNA
 #residues 1-466 #label VOL
 #cross-references GDB:579852
 #note the authors translated the codon GCC for residue 427 as Leu

FEATURE
 1-21 domain signal sequence status predicted label SIG\N
 22-466 product glucose-dependent insulinotropic protein receptor status predicted label MAT
 SUMMARY length 466 molecular-weight 53142 checksum 1170

Query Match
 Best Local Similarity 100.04; Pred. No. 4.08e-11;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 162 FRLNCTNRYH 173
 QY 169 FRLNCTNRYH 180

RESULT 16
 ENTRY title
 ALTERNATE_NAMES
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCES
 #authors
 #journal

#title Cloning, functional expression, and chromosomal localization of the human pancreatic islet glucose-dependent insulinotropic polypeptide receptor.
 #accession J37411
 #status preliminary; translated from GDB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-466 #label R88
 #cross-references EMBL:X81932; NID:G1030050; PID:G1030051
 SUMMARY length 491 molecular-weight 55650 checksum 2199

Query Match
 Best Local Similarity 100.04; Pred. No. 4.08e-11;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 161 FRLNCTNRYH 172
 QY 169 FRLNCTNRYH 180

RESULT 17
 ENTRY title
 ALTERNATE_NAMES
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCES
 #authors
 #journal
 #title
 #accession
 #molecule_type mRNA
 #residues 1-477 #label MAC

GENETICS
 #name GDB:GCCR, GCR
 #cross-references GDB:304516; OMIM:138033
 #map_position 17q25-17q25
 #length 477
 #checksum 17425

FEATURE
 22-477 domain signal sequence status predicted label SIG\N
 143-166 product glucagon receptor status predicted label MAT\N
 174-194 domain transmembrane status predicted label TM\N
 266-285 domain transmembrane status predicted label TM\N
 302-323 domain transmembrane status predicted label TM\N
 332-369 domain transmembrane status predicted label TM\N
 386-403 domain transmembrane status predicted label TM\N
 46.39.74.78 binding site carbohydrate (Aa) (covalent) status predicted

SUMMARY length 477 molecular-weight 54008 checksum 53

Query Match
 Best Local Similarity 100.04; Pred. No. 2.66e-06
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 243 LVEGLYHNC 252
 QY 255 LVEGLYHNC 264

RESULT 18
 ENTRY title
 ALTERNATE_NAMES
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCES
 #authors
 #submission
 #accession
 #status preliminary
 #molecule_type mRNA
 #residues 1-477 #label SV0
 #cross-references EMBL:422735; NID:G311228; PID:G311229

Summary
 length 381 checksum 7833

Query Match
 Best Local Similarity 100.04; Pred. No. 1.7e-13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 77 LFVSPMRA 85
 QY 183 LFVSPMRA 191

RESULT 19
 ENTRY title
 ALTERNATE_NAMES
 ORGANISM
 DATE
 ACCESSIONS
 REFERENCES
 #authors
 #journal

Tue Nov 24 08:11:00 1998 US-08-468-011A-2.rpr

title The VIP(2) receptor: molecular characterization of a cDNA encoding a novel receptor for vasoactive intestinal peptide.

accession J39068

entry J39068

type 1-437 #label LUT

residues 1-437

cross-references EMBL:21885; NID:941188; PID:941189

keywords G protein-coupled receptor; intestine; transmembrane protein

summary length 437; molecular-weight 49552; checksum 7187

Query Match 1.7% Score 9; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 LECTRNVIH 161
QY 172 LECTRNVIH 180

RESULT 20

ENTRY J39068

TITLE PACAP/VIP receptor (PACAPR-3) - mouse

ORGANISM Mus musculus

DATE 25-Oct-1996

ACCESSIONS A53471; J00185

REFERENCE A53471; J00185

authors Gonoi, T.; Miyazaki, J.; Saito, S.; Fujii, Y.; Kato, T.; Yoshida, K.; Minata, M.; Minano, M.

journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2679-2683

title Cloning and functional characterization of a third pituitary adenylate cyclase activating polypeptide receptor subtype expressed in rat lung.

cross-references NID:9419806

accession A53471

entry A53471

type Preliminary: translated from GB/EMBL/DBJ

residues 1-437 #label RES

cross-references GB:D28132; NID:9473721; PID:9496376

experimental_source strain C57BL/6

length 437; molecular-weight 49473; checksum 7275

Query Match 1.7% Score 9; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 153 LECTRNVIH 161
QY 172 LECTRNVIH 180

Tue Nov 24 08:11:00 1998

US-08-468-011A-2.rpr

entry J02463

type complete

title Vasoactive intestinal peptide receptor - human

organism Homo sapiens

date 21-Feb-1995

sequence_revision 05-Apr-1995

text_change 10-Sep-1997

accessions J02463

reference J02463

authors Suda, M.; Tatemoto, M.; Van Ranspaalbeigh, J.; Goossens, J.F.; De Neef, P.; Waelbroeck, W.; Bobbrecq, P.

journal Biochem. Biophys. Res. Commun. (1994) 205:1617-1624

title Molecular cloning and functional characterization of a human VIP(2) receptor from SUP-T1 lymphoblasts.

accession J02463

entry J02463

type mRNA

residues 1-438 #label SVO

cross-references GB:D5656; NID:9550477; PID:9550478

experimental_source cell line

keywords glycoprotein; intestine; receptor; transmembrane protein

feature 130-150 domain transmembrane status predicted label TM1
150-178 domain transmembrane status predicted label TM2
178-206 domain transmembrane status predicted label TM3
206-234 domain transmembrane status predicted label TM4
234-262 domain transmembrane status predicted label TM5
262-304 domain transmembrane status predicted label TM6
304-322 domain transmembrane status predicted label TM7
322-349 domain transmembrane status predicted label TM8
349-377 domain transmembrane status predicted label TM9
377-405 domain transmembrane status predicted label TM10
405-438 binding site carbohydrate (Asn) (covalent) status predicted

summary length 438; molecular-weight 49503; checksum 8054

Query Match 1.7% Score 9; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 LECTRNVIH 162
QY 172 LECTRNVIH 180

RESULT 22

ENTRY G02822

TITLE VIP2 receptor - human

ORGANISM Homo sapiens

DATE 21-Dec-1996

sequence_revision 06-Jun-1997

text_change 06-Jun-1997

accessions G02822

reference H01736

authors Luts, E.M.

submission submitted to the EMBL Data Library, January 1996

Tue Nov 24 08:11:00 1998 US-08-468-011A-2.rpr

accession G02822

entry G02822

type Preliminary: translated from GB/EMBL/DBJ

residues 1-438 #label LUT

cross-references EMBL:X50597; NID:91160469

genetics VIP2r

summary length 438; molecular-weight 49478; checksum 7593

Query Match 1.7% Score 9; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 LECTRNVIH 162
QY 172 LECTRNVIH 180

RESULT 23

ENTRY A46172

TITLE glucagon-like peptide 1 receptor - rat

ALTERNATE_NAMES GLP-1 receptor

ORGANISM Rattus norvegicus

DATE 27-Feb-1997

sequence_revision 10-Nov-1994

text_change 27-Feb-1997

accessions A46172; I53420; I59231

reference A46172

authors Loh, B.

journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:8641-8645

title Expression cloning of the pancreatic beta cell receptor for the glucagon-like peptide 1.

cross-references NID:9240952

accession A46172

entry A46172

type Preliminary

residues 1-463 #label THO

cross-references GB:D304326; PID:937868

experimental_source pancreatic islet cell

note sequence extracted from MCB1 backbone

reference I53420

authors Loh, B.; Goke, R.; Fehrmann, H.C.; Richter, G.; Exner, C.

journal Exp. Clin. Endocrinol. (1994) 102:341-347

title Molecular cloning of a cDNA encoding for the GLP-1 receptor expressed in rat lung.

cross-references NID:9311298

accession I53420

entry I53420

type Preliminary: translated from GB/EMBL/DBJ

residues 1-463 #label RES

cross-references GB:D304326; PID:937868

Tue Nov 24 08:11:00 1998

US-08-468-011A-2.rpr

entry J02463

type complete

title Vasoactive intestinal peptide receptor - human

organism Homo sapiens

date 21-Feb-1995

sequence_revision 05-Apr-1995

text_change 10-Sep-1997

accessions J02463

reference J02463

authors Suda, M.; Tatemoto, M.; Van Ranspaalbeigh, J.; Goossens, J.F.; De Neef, P.; Waelbroeck, W.; Bobbrecq, P.

journal Biochem. Biophys. Res. Commun. (1994) 205:1617-1624

title Molecular cloning and functional characterization of a human VIP(2) receptor from SUP-T1 lymphoblasts.

accession J02463

entry J02463

type mRNA

residues 1-438 #label SVO

cross-references GB:D5656; NID:9550477; PID:9550478

experimental_source cell line

keywords glycoprotein; intestine; receptor; transmembrane protein

feature 130-150 domain transmembrane status predicted label TM1
150-178 domain transmembrane status predicted label TM2
178-206 domain transmembrane status predicted label TM3
206-234 domain transmembrane status predicted label TM4
234-262 domain transmembrane status predicted label TM5
262-304 domain transmembrane status predicted label TM6
304-322 domain transmembrane status predicted label TM7
322-349 domain transmembrane status predicted label TM8
349-377 domain transmembrane status predicted label TM9
377-405 domain transmembrane status predicted label TM10
405-438 binding site carbohydrate (Asn) (covalent) status predicted

summary length 438; molecular-weight 49503; checksum 8054

Query Match 1.7% Score 9; DB 2; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 154 LECTRNVIH 162
QY 172 LECTRNVIH 180

RESULT 24

ENTRY S71624

TITLE glucagon-like peptide 1 receptor, pancreatic - human

ALTERNATE_NAMES GLP-1 receptor

ORGANISM Homo sapiens

DATE 27-Nov-1997

sequence_revision 12-Dec-1997

text_change 27-Nov-1997

accessions S71624

reference S71624

authors Wei, Y.; Mojsov, S.

journal FEBS Lett. (1995) 358:219-224

title Identification and characterization of the human receptor for glucagon-like peptide-1: brain, heart and pancreatic forms have the same deduced amino acid sequences.

accession S71624

entry S71624

type cDNA

residues 1-463 #label WBI

cross-references EMBL:U10037

experimental_source clone HPC10; pancreas

description stimulates glucose-induced insulin secretion

keywords G protein-coupled receptor; glycoprotein; pancreas; transmembrane protein

feature 130-150 domain transmembrane status predicted label TM1
150-178 domain transmembrane status predicted label TM2
178-206 domain transmembrane status predicted label TM3
206-234 domain transmembrane status predicted label TM4
234-262 domain transmembrane status predicted label TM5
262-304 domain transmembrane status predicted label TM6
304-322 domain transmembrane status predicted label TM7
322-349 domain transmembrane status predicted label TM8
349-377 domain transmembrane status predicted label TM9
377-405 domain transmembrane status predicted label TM10
405-438 binding site carbohydrate (Asn) (covalent) status predicted

summary length 463; molecular-weight 53010; checksum 515

Query Match 1.7% Score 9; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 4.55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Tue Nov 24 08:11:00 1998

[illegible]

```

#status      preliminary
#molecule_type mRNA
#residues    1-117.VV.13-136.F.189-259,F'.261-483.#label EYL
COMMENT      Intracellular levels of cyclic adenosine monophosphate raise
              intracellular levels of cyclic adenosine monophosphate.
KEYWORDS     glycoprotein; receptor; transmembrane protein
FEATURES
  1..148      #domain transmembrane status predicted label TM1
  177-198     #domain transmembrane status predicted label TM2
  228-246     #domain transmembrane status predicted label TM3
  268-287     #domain transmembrane status predicted label TM4
  305-325     #domain transmembrane status predicted label TM5
  351-373     #domain transmembrane status predicted label TM6
  388-407     #domain transmembrane status predicted label TM7
  63.87,115   binding site carbohydrate (Aan) (covalent) status
               predicted
SUMMARY      length 493 #molecular-weight 53025 #checksum 765
               1.74; Score 8; DB 2; Length 463;
               Query Match Local similarity 100.0%; Pred. No. 4.5se=04;
               Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db          172 LCTRINR180
QY          172 LCTRINR180
|||||
|||
RESULT      26      I84494      type complete
ENTRY        Glucagon-like peptide-1 receptor - human
TITLE        GLP-1 Receptor (GLP-1R), Human
AUTHOR       O'Sang-Aug-1996 sequence_revision 02-Aug-1996 feat_change
DATE         23-Aug-1997
ACCESSION    I84494
VERSION      18655
REFERENCES   Terasaki, B.; Porret, A.; Buehler, L.; Deng, S.; Korel, P.;
              Widmann, C.
              Diabetes (1993) 42:1678-1682
#journal     Cloning and functional expression of the human islet GLP-1
#title       receptor (glucagon-like peptide-1 receptor).
#keywords     receptor; glucagon; insulin antagonist of the receptor.
#cross-references MIDB:9400986
accession    I84494
#status      Preliminary; translated from GB/EMBL/DDBJ
#molecule_type cDNA
#residues    1-463 #label RES
#features     {}
#cross-references EMBL:U01104; NID:g405081; PID:g405082
#gene        GDB:GLP1R
#organism     Homo sapiens
#map_position 6621-6921
GENETICS

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Tue Nov 24 08:11:00 1998

```

SUMMARY          #length 467 #molecular-weight 53232 #checksum 4520

Query Match      1.74; Score 9; DB 2; Length 467;
Best local similarity 100.0%; Pval 0; 4.55e-04;
Matches 0; Conservative 0; Identical 0; Gaps 0;

Db 191 LFVSMFLA 199
|||||
Qy 193 LFVSMFLA 191

RESULT 28
ENTRY          JQ1957 #type complete
ALTERNATE_NAMES GP-1 receptor homolog, hepatic
ORGANISM       #formal_name Rattus norvegicus #common_name Norway rat
DATE           30-Sep-1993 #sequence_revision 10-Sep-1993 #text_change
ACCESSIONS     JQ1957 #accession
AUTHORS        JQ1957 #author
REFERENCE      Svoboda, M.; Ciccarelli, E.; Tastenoy, M.; Guvian, A.;
                Blivenat, M.; Charlebois, J. 1993 191-479-486
                #journal J Biol Chem 268:191-479-486
                #title Small introns in a hepatic cDNA encoding a new glucocorticoid-
                peptide 1-type receptor.
                #accession JQ1957
                #molecule_type mRNA
                #date 1993
                #cross-references GB X68692
                #experimental_source liver

REFERENCE      J6211 #type complete
AUTHORS       Fagan, L.J.; Lok, S.; Rosenberg, G.B.; Smith, P.A.; Grant,
                P.J.; Blaser, S.; Bonnichsen, P.; Kujder, A.;
                Strydom, C.A.; O'Hara, P.J.; Foster, D.; Walker,
                K.M.; Chen, L.H.J.; McKernan, P.A.; Kindasvogel, W.
                #journal Science (1993) 259:1614-1618
                #title Molecular cloning and signaling properties of the rat
                glucocorticoid receptor.
                #cross-references MIMD-93206096
                #accession A46211
                #status Preliminary; nucleic acid sequence not shown; not
                completed with conceptual translation

#molecule_type mRNA
#residues 1-37, 'W', '38-215', 'W', '217-323', 'V', '325-485 #label JEL
#experimental_source liver
#description Sequence extracted from NOBI backbone (NCBIPI:127705)
#keywords G protein-coupled receptor; glycoprotein; liver;
          phosphoprotein; transmembrane protein

GENETICS
132(3): 168(2); 220(2): 407(3)
#introns
#keywords
FEATURE

```

144-167
175-194
245-239
246-281
305-324
352-370
389-405
47-60,75,79
432

domain transmembrane status predicted label TM1
domain transmembrane status predicted label TM2
domain transmembrane status predicted label TM3
domain transmembrane status predicted label TM4
domain transmembrane status predicted label TM5
domain transmembrane status predicted label TM6
domain transmembrane status predicted label TM7
binding site carbohydrate (am) (covalent) status
predicted

SUMMARY length 485 molecular-weight 54927 checksum 6596

Query Match 1.7% Score 9; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 4,55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 170 LNCRTNVIH 178
QY 172 LNCRTNVIH 180

RESULT 29
ENTRY
TITLE
ORGANISM
DATE

JC4363
glucagon receptor - mouse
Mus musculus
08-Feb-1996

ALTERNATE_NAMES
ORGANISM
DATE

JC4363
glucagon receptor - mouse
Mus musculus
08-Feb-1996

REFERENCE
AUTHORS
TITLE

Burrell, R. J., J. J. Charron, M. J.
Cloning and sequence analysis of the murine glucagon
receptor-encoding gene.

JC4363
accession
molecule-type mRNA
#molecule-weight 54927
#cross-references GB:L18612

COMMENT This receptor is a plasma membrane glycoprotein that belongs to a
subfamily of peptide hormone receptors. It plays a major role in
the regulation of glucose metabolism by stimulating
the release of insulin from the beta cells of the pancreas.
secretion by beta cells.

GENETICS
SYNTE
AUTHORS
KEYWORDS
FEATURE
1-27
29-405

domain signal sequence status predicted label SIG
product glucagon receptor status predicted label SIG

RESULT 31
ENTRY
TITLE
ORGANISM
DATE

A48204
pituitary adenylyl cyclase-activating polypeptide type I
receptor precursor - rat
Rattus norvegicus
07-Oct-1994

ALTERNATE_NAMES
ORGANISM
DATE

A48204
pituitary adenylyl cyclase-activating polypeptide type I
receptor precursor - rat
Rattus norvegicus
07-Oct-1994

REFERENCE
AUTHORS
TITLE

Pisegna, J. R., Wank, S. A.,
Cloning and sequence analysis of the rat pituitary
adenylyl cyclase-activating polypeptide type I receptor.

A48204
accession
molecule-type Preliminary
#molecule-weight 54416
#cross-references GB:L1680; PID:g347941

KEYWORDS
FEATURE
1-191
20-495

domain signal sequence status predicted label SIG
product pituitary adenylyl cyclase-activating
polypeptide type I receptor status predicted label
SIG

SUMMARY length 495 molecular-weight 54416 checksum 7886

Query Match 1.7% Score 9; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 4,55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 191 LFNVSPLERA 199
QY 183 LFNVSPLERA 191

RESULT 32
ENTRY
TITLE
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 3
PACAP receptor
Mus musculus
19-Mar-1997

ALTERNATE_NAMES
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 3
PACAP receptor
Mus musculus
19-Mar-1997

REFERENCE
AUTHORS
TITLE

Spengler, D.; Weber, C.; Pantaloni, C.; Holboer, F.;
Cloning and sequence analysis of the murine glucagon
receptor-encoding gene.

S39061
accession
molecule-type mRNA
#molecule-weight 54927
#cross-references GB:L18612

COMMENT This receptor is a plasma membrane glycoprotein that belongs to a
subfamily of peptide hormone receptors. It plays a major role in
the regulation of glucose metabolism by stimulating
the release of insulin from the beta cells of the pancreas.
secretion by beta cells.

GENETICS
SYNTE
AUTHORS
KEYWORDS
FEATURE
1-27
29-405

domain signal sequence status predicted label SIG
product glucagon receptor status predicted label SIG

145-168
176-196
245-239
246-281
305-324
352-370
389-405
47-60,65,75,79,
118

domain transmembrane status predicted label TM1
domain transmembrane status predicted label TM2
domain transmembrane status predicted label TM3
domain transmembrane status predicted label TM4
domain transmembrane status predicted label TM5
domain transmembrane status predicted label TM6
domain transmembrane status predicted label TM7
binding site carbohydrate (am) (covalent) status
predicted

SUMMARY length 485 molecular-weight 54872 checksum 5999

Query Match 1.7% Score 9; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 4,55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 170 LNCRTNVIH 178
QY 172 LNCRTNVIH 180

RESULT 30
ENTRY
TITLE
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 5
PACAP receptor
Mus musculus
19-Mar-1997

ALTERNATE_NAMES
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 5
PACAP receptor
Mus musculus
19-Mar-1997

REFERENCE
AUTHORS
TITLE

Spengler, D.; Weber, C.; Pantaloni, C.; Holboer, F.;
Cloning and sequence analysis of the murine glucagon
receptor-encoding gene.

S39061
accession
molecule-type mRNA
#molecule-weight 54927
#cross-references GB:L18612

COMMENT This receptor is a plasma membrane glycoprotein that belongs to a
subfamily of peptide hormone receptors. It plays a major role in
the regulation of glucose metabolism by stimulating
the release of insulin from the beta cells of the pancreas.
secretion by beta cells.

GENETICS
SYNTE
AUTHORS
KEYWORDS
FEATURE
1-27
29-405

domain signal sequence status predicted label SIG
product glucagon receptor status predicted label SIG

RESULT 31
ENTRY
TITLE
ORGANISM
DATE

A48204
pituitary adenylyl cyclase-activating polypeptide type I
receptor precursor - rat
Rattus norvegicus
07-Oct-1994

ALTERNATE_NAMES
ORGANISM
DATE

A48204
pituitary adenylyl cyclase-activating polypeptide type I
receptor precursor - rat
Rattus norvegicus
07-Oct-1994

REFERENCE
AUTHORS
TITLE

Pisegna, J. R., Wank, S. A.,
Cloning and sequence analysis of the rat pituitary
adenylyl cyclase-activating polypeptide type I receptor.

A48204
accession
molecule-type Preliminary
#molecule-weight 54416
#cross-references GB:L1680; PID:g347941

KEYWORDS
FEATURE
1-191
20-495

domain signal sequence status predicted label SIG
product pituitary adenylyl cyclase-activating
polypeptide type I receptor status predicted label
SIG

SUMMARY length 495 molecular-weight 54416 checksum 8114

Query Match 1.7% Score 9; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 4,55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 191 LFNVSPLERA 199
QY 183 LFNVSPLERA 191

RESULT 32
ENTRY
TITLE
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 3
PACAP receptor
Mus musculus
19-Mar-1997

ALTERNATE_NAMES
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 3
PACAP receptor
Mus musculus
19-Mar-1997

REFERENCE
AUTHORS
TITLE

Spengler, D.; Weber, C.; Pantaloni, C.; Holboer, F.;
Cloning and sequence analysis of the murine glucagon
receptor-encoding gene.

S39061
accession
molecule-type mRNA
#molecule-weight 54927
#cross-references GB:L18612

COMMENT This receptor is a plasma membrane glycoprotein that belongs to a
subfamily of peptide hormone receptors. It plays a major role in
the regulation of glucose metabolism by stimulating
the release of insulin from the beta cells of the pancreas.
secretion by beta cells.

GENETICS
SYNTE
AUTHORS
KEYWORDS
FEATURE
1-27
29-405

domain signal sequence status predicted label SIG
product glucagon receptor status predicted label SIG

RESULT 33
ENTRY
TITLE
ORGANISM
DATE

S36114
pituitary adenylyl cyclase-activating polypeptide type I
receptor - rat
Rattus norvegicus
06-Feb-1995

ALTERNATE_NAMES
ORGANISM
DATE

S36114
pituitary adenylyl cyclase-activating polypeptide type I
receptor - rat
Rattus norvegicus
06-Feb-1995

REFERENCE
AUTHORS
TITLE

J. A. Lutz, E. M. West, K. M. Fink, G. Hammar, A. J.
Molecular cloning and expression of a cDNA encoding a
receptor for pituitary adenylyl cyclase activating
polypeptide (PACAP).

S36114
accession
molecule-type mRNA
#molecule-weight 54416
#cross-references GB:L1680; PID:g347941

KEYWORDS
FEATURE
1-191
20-495

domain signal sequence status predicted label SIG
product pituitary adenylyl cyclase-activating
polypeptide type I receptor status predicted label
SIG

SUMMARY length 495 molecular-weight 54416 checksum 7886

Query Match 1.7% Score 9; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 4,55e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 191 LFNVSPLERA 199
QY 183 LFNVSPLERA 191

RESULT 34
ENTRY
TITLE
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 3
PACAP receptor
Mus musculus
19-Mar-1997

ALTERNATE_NAMES
ORGANISM
DATE

S39061
pituitary adenylyl cyclase activating-peptide receptor form 3
PACAP receptor
Mus musculus
19-Mar-1997

REFERENCE
AUTHORS
TITLE

Spengler, D.; Weber, C.; Pantaloni, C.; Holboer, F.;
Cloning and sequence analysis of the murine glucagon
receptor-encoding gene.

S39061
accession
molecule-type mRNA
#molecule-weight 54927
#cross-references GB:L18612

COMMENT This receptor is a plasma membrane glycoprotein that belongs to a
subfamily of peptide hormone receptors. It plays a major role in
the regulation of glucose metabolism by stimulating
the release of insulin from the beta cells of the pancreas.
secretion by beta cells.

GENETICS
SYNTE
AUTHORS
KEYWORDS
FEATURE
1-27
29-405

domain signal sequence status predicted label SIG
product glucagon receptor status predicted label SIG


```

QY 183 LFVSMFLRA 191

RESULT 37
ENTRY
TITLE corticotropin-releasing factor receptor subtype 2 - rat
ORGANISM Rattus norvegicus
DATE 02-Jul-1996
ACCESSIONS A55610
AUTHORS Lovenberg, T.W.; Liaw, C.M.; Grigoriadis, D.E.; Clavenger,
REFERENCE Proc. Natl. Acad. Sci. U.S.A. 93:13440 (1996)
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (1996) 93:13440
TITLE Cloning and characterization of a functionally distinct
corticotropin-releasing factor receptor subtype from rat
brain: published erratum appears in Proc Natl Acad Sci U S
A 95:14662 (1998)
ACROSS-REFERENCES MIMD:9514662
ACCESSION A55610
STATUS preliminary
MOLECULE_TYPE DNA
RESIDUES 1-411
ACROSS-REFERENCES EMBL:U16253; NID:9644771; PID:9644772
GENETICS CR22H
GENE CR22H
SUMMARY length 411 molecular-weight 47706 checksum 7683
Query Match 1.5%; Score 8; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.53e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 SPOGPFVS 356
QY 403 SPOGPFVS 410

RESULT 38
ENTRY
TITLE hypothetical protein - Synchococcus sp. (PCC 7002)
ORGANISM Synchococcus sp.
DATE 19-Mar-1997
ACCESSIONS S18125
AUTHORS Brand, S.N.; Tan, X.; Widger, W.R.
REFERENCE submitted to the EMBL Data Library, November 1991
JOURNAL The cloning and sequencing of the petdD operon from the
SYNCHOCYCLUS bacterium, Synchococcus PCC 7002.
ACCESSION S18125

```

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ORGANISM Rattus norvegicus
DATE 26-Jul-1996
ACCESSIONS I58144
AUTHORS Chang, C.P.; Pearce, R.V.; O'Connell, S.; Rosenfeld, M.G.
REFERENCE Neuron (1993) 11:1187-1195
JOURNAL Identification of a seven transmembrane helix receptor for
TITLE corticotropin-releasing factor and sauvagine in mammalian
brain
ACROSS-REFERENCES MIMD:9409969
ACCESSION I58144
STATUS preliminary
MOLECULE_TYPE RNA
RESIDUES 1-415
ACROSS-REFERENCES GB:L25438; NID:9450298; PID:9457615
SUMMARY length 415 molecular-weight 47842 checksum 3934
Query Match 1.5%; Score 8; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.53e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 353 SPOGPFVS 360
QY 403 SPOGPFVS 410

RESULT 41
ENTRY
TITLE corticosteroid receptor precursor, heart-specific - mouse
ORGANISM Mus musculus
DATE 28-Feb-1997
ACCESSIONS A56726
AUTHORS Stenel, P.; Kenterson, R.; Yeung, W.; Cone, R.D.;
REFERENCE Mol. Endocrinol. (1995) 9:637-645
JOURNAL Identification of a novel murine receptor for
TITLE corticotropin-releasing hormone expressed in the heart.
ACCESSION A56726
STATUS preliminary
MOLECULE_TYPE mRNA
RESIDUES 1-430
ACROSS-REFERENCES GB:U19939; NID:9806763; PID:9806764
KEYWORDS heart
SUMMARY length 430 molecular-weight 49682 checksum 7906
Query Match 1.5%; Score 8; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 5.53e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

STATUS preliminary
MOLECULE_TYPE DNA
RESIDUES 1-411
ACROSS-REFERENCES EMBL:X83049; NID:938062; PID:938065
SUMMARY length 411 molecular-weight 45418 checksum 5449
Query Match 1.5%; Score 8; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 5.53e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 LVLVLPFG 22
QY 366 LVLVLPFG 373

RESULT 39
ENTRY
TITLE corticotropin-releasing hormone receptor - mouse
ORGANISM Mus musculus
DATE 07-Oct-1994
ACCESSIONS S39535
AUTHORS Varga, M.; Laurent, P.; Lefort, S.; Chalou, P.; Lelias, J.M.;
REFERENCE FEBS Lett. (1993) 335:1-5
JOURNAL Primary structure and functional expression of mouse
TITLE pituitary and human brain corticotropin releasing factor
receptor cDNAs.
ACCESSION S39535
STATUS preliminary
MOLECULE_TYPE RNA
RESIDUES 1-415
ACROSS-REFERENCES EMBL:X72105; NID:9436120; PID:9436121
SUMMARY the sequence from Fig. 1 is inconsistent with that from
Fig. 3 in having an additional Tyr after 84-Tyr
G protein-coupled receptor; transmembrane protein
length 415 molecular-weight 47769 checksum 3734
Query Match 1.5%; Score 8; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.53e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 353 SPOGPFVS 360
QY 403 SPOGPFVS 410

RESULT 40
ENTRY
TITLE corticotropin-releasing factor receptor - rat

```

```

Db 368 SPOGPFVS 375
QY 403 SPOGPFVS 410

RESULT 42
ENTRY
TITLE sauvagine/corticotropin-releasing factor receptor - mouse
ORGANISM Mus musculus
DATE 02-Jul-1996
ACCESSIONS I49279
AUTHORS Kikimoto, T.; Pearce, R.V.
REFERENCE Proc. Natl. Acad. Sci. U.S.A. (1995) 92:1108-1112
JOURNAL A sauvagine/corticotropin-releasing factor receptor expressed
TITLE in heart and skeletal muscle (published erratum appears in
Proc. Natl. Acad. Sci. U.S.A. 1995 Apr 25;92(9):4074).
ACROSS-REFERENCES MIMD:9516678
ACCESSION I49279
STATUS preliminary
MOLECULE_TYPE RNA
RESIDUES 1-415
ACROSS-REFERENCES EMBL:U21729; NID:9717137; PID:9717138
SUMMARY length 411 molecular-weight 49924 checksum 9354
Query Match 1.5%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 5.53e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 369 SPOGPFVS 376
QY 403 SPOGPFVS 410

RESULT 43
ENTRY
TITLE CRF receptor - mouse
ORGANISM Mus musculus
DATE 02-Jul-1996
ACCESSIONS I49149
AUTHORS Perrin, M.; Donaldson, C.; Chen, R.; Blount, A.; Berggren,
REFERENCE T.; Bilezikian, J.P.; Savchenko, S.; Yalcin, M.
JOURNAL Identification of a second corticotropin-releasing factor
TITLE receptor gene and characterization of a cDNA expressed in
heart.
ACROSS-REFERENCES MIMD:95224061

```

```

accession      I49149
status         preliminary; translated from GB/EML/DB8J
#molecule_type RNA
#residues       1-431 #label RES
#cross-references DB/JD/PD/727354, P/D/G727355
#length        431 #molecular-weight 49923 #checksum 22

SUMMARY
Query Match          J.D.5; Score 8; DB 2; Length 431;
                        # mismatches 0; Indels 0; Gaps 0;
                        Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    369 SPOGPFWS 376
Oy    403 SPOGPFWS 410

RESULT 44
TITLE   A48260 type complete
        corticotropin receptor, long splice form - human
ALTERNATE_NAMES corticotropin binding protein; corticotropin releasing
                 factor receptor; corticotropin releasing hormone receptor
ORGANISM Homo sapiens common name
DATE     28-Aug-1997
ACCESSIONS I60975; A48260; S39534
REFERENCE   I48260 Lewis, K.A.; Perrin, M.H.; Vale, W.W.
           Proc. Natl. Acad. Sci. U.S.A. (1993) 90:8967-8971
           Expression cloning of a human corticotropin-releasing factor
           receptor.
CROSS-REFERENCES DB/JD/PD/94022396
#molecule_type RNA
#residues       444 #label RES
#cross-references DB/JD/PD/908491; P/D/G408692
#experimental_source Cushing corticotropic cell tumor
#length        444
#checksum      28620
#status        preliminary; translated from GB/EML/DB8J

#molecule_type mRNA
#residues       1745,175-444 #label RE2
#cross-references DB/J21332; NID/S408489; PID/G408690
#authors       Vite, N.; Laurent, P.; Lafont, S.; Chalou, P.; Lelias, J.M.;
               FEMS Lett. (1993) 335:1-5
               Laput, O.; Ferrara, P.
#journal        Primary structure and functional expression of mouse
               pituitary and human brain corticotropin releasing factor
               receptors.
#title
#status        preliminary

```

Tue Nov 24 08:11:00 1998

```

GENETICS      SCD-PCV7
$macros=references SGD:S0000859; MIPS:YER056c
map_position 5R
CLASSIFICATION superfamily cytochrome/purine transport protein
KEYWORDS        glycoprotein, transmembrane protein
FEATURE
  99-119    alpha domain transmembrane status predicted label TM\
  124-142    alpha domain transmembrane status predicted label TM\
  150-168    alpha domain transmembrane status predicted label TM\
  199-221    alpha domain transmembrane status predicted label TM\
  257-277    alpha domain transmembrane status predicted label TM\
  301-320    alpha domain transmembrane status predicted label TM\
  324-343    alpha domain transmembrane status predicted label TM\
  398-419    alpha domain transmembrane status predicted label TM\
  456-485    alpha domain transmembrane status predicted label TM\
  460-485    binding site carbohydrate (Aan) (covalent) status
              predicted
length 537 molecular-weight 58201 checksum 5327

SUMMARY
Query Match          1.5% Score 8: DB 1: Length 533:
Best Local Similarity 100.0%: Pred. No. 5.35e-02;
Matches            0: Conservative           0: Mismatches           0: Indels           0: Gaps           0:

Db       133 LIFWAFS 140
Qy       264 LIFWAFS 271

RESULT      46
ENTRY
TITLE
AUTHOR
ORGANISM
DATE
ACCESSIONS
REFERENCE
authors
submitter
release
status
molecule-type preliminary
sequence-length 50
accession-number F59
classification superfamily cytochrome/purine transport protein
keywords        glycoprotein, transmembrane protein
length 50 checksum 6564

CLASSIFICATION superfamily cytochrome/purine transport protein
KEYWORDS        glycoprotein, transmembrane protein
length 50 checksum 6564

Query Match          1.3% Score 7: DB 2: Length 50:
Best Local Similarity 100.0%: Pred. No. 4.35e+00;

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Tue Nov 24 08:11:00 1998

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 12 KIRAST 18
      |||||
QY 360 KIRAST 366

RESULT 47
ENTRY ZBR74       type complete
AUTHOR Broida, J.; Abelson, J.
JOURNAL Mol. Biol. (1987), 195, 545-563
TITLE Superfamily phage T4 gene 578 protein
NOTE host Escherichia coli
DATE 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change
ACCESSION A04311 #seq-no:1997
REFERENCE A92919
AUTHORA Broida, J.
JOURNAL Mol. Biol. (1987), 195, 545-563
TITLE Superfamily phage T4 gene 578 protein
NOTE bacteriophage T4 trnaA region.
#cross-references M01D:86037230
ACCESSION A04311 #seq-no:1997
AUTHOR Broida, J.
TITLE Superfamily phage T4 gene 578 protein
#residues 1-152 #label BRO
#cross-references GB:J02516; GB:J02517;
GB:J03016; GB:J02511; GB:J02516; GB:J02517;
GB:V00861; GB:V00862; NID:g15386; PID:g15389

GENETICS 578
ENTRY ZBR74       type complete
AUTHOR Broida, J.; Abelson, J.
JOURNAL Mol. Biol. (1987), 195, 545-563
TITLE Superfamily phage T4 gene 578 protein
NOTE host Escherichia coli
DATE 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change
ACCESSION A04311 #seq-no:1997
REFERENCE A92919
AUTHORA Broida, J.
JOURNAL Mol. Biol. (1987), 195, 545-563
TITLE Superfamily phage T4 gene 578 protein
NOTE bacteriophage T4 trnaA region.
#cross-references M01D:86037230
ACCESSION A04311 #seq-no:1997
AUTHOR Broida, J.
TITLE Superfamily phage T4 gene 578 protein
#residues 1-152 #label BRO
#cross-references GB:J02516; GB:J02517;
GB:J03016; GB:J02511; GB:J02516; GB:J02517;
GB:V00861; GB:V00862; NID:g15386; PID:g15389

SUMMARY
length 152 #molecular-weight 17244 #scheKaum 2170
138; Score 7; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 4.35e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 80 STUWVL 86
      |||||
QY 364 STUWVL 370

RESULT 48
ENTRY ZBR74       type complete
AUTHOR Broida, J.; Abelson, J.
JOURNAL Mol. Biol. (1987), 195, 545-563
TITLE Superfamily phage T4 gene 578 protein
NOTE host Escherichia coli
DATE 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change
ACCESSION A04311 #seq-no:1997
REFERENCE A92919
AUTHORA Broida, J.
JOURNAL Mol. Biol. (1987), 195, 545-563
TITLE Superfamily phage T4 gene 578 protein
NOTE bacteriophage T4 trnaA region.
#cross-references M01D:86037230
ACCESSION A04311 #seq-no:1997
AUTHOR Broida, J.
TITLE Superfamily phage T4 gene 578 protein
#residues 1-152 #label BRO
#cross-references GB:J02516; GB:J02517;
GB:J03016; GB:J02511; GB:J02516; GB:J02517;
GB:V00861; GB:V00862; NID:g15386; PID:g15389

```

[illegible]

```

#crosses=references PMID:97061201 potential protein-coding regions.
#accession S75157
#status nucleic acid sequence not shown; translation not shown
#accession S75157
#residue_type 1-190 #label KAN
#crosses=references EMBL:D90903; NID:g1652127; PID:d1017804; PID:g165214
#note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996

GENETICS
#gene
#fbp
#start_codon GTG
#summary length 190 #molecular_weight 19548 #checksum 9434

Query Match 1.3% Score 7; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 4; 36e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 PAFVAA 41
|||||
QY 287 PAFVAA 293

Search completed: Mon Nov 23 13:40:28 1998
Job time : 105 secs.

```



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*****
WOLF
(TM)

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MPHSPR_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Nov 23 13:36:01 1998; Mapair time 14.69 Seconds
595.885 Million cell updates/sec

Tabular output not generated.

>US-08-468-011A-2
Title:
Description:
Perfect Score: 541
Sequence: 1 HAWKASLHFWGHWKAGSCL.....DDLWKGKPNWSPHDTGC 541

Scoring table:
TABLE unprotable
Gap 60
131972 seqs, 16180680 residues
Post-processing: Minimum Match 0%
Waiting first: 1000 summaries

Database:
a-genecore32
2-part1 2-part2 3-part3 4-part4 5-part5 6-part6 7-part7
8-part8 9-part9 10-part10 11-part11 12-part12 13-part13
14-part14 15-part15 16-part16 17-part17 18-part18 19-part19
20-part20 21-part21 22-part22 23-part23 24-part24
25-part25 26-part26 27-part27 28-part28
29-part29

Statistics:
Mean 3.007; Variance 0.698; scale 4.311

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```

48	1	5	415	18	W04519	Human corticotropin r	1,194+02
49	8	1,5	416	18	R65921	Human corticotropin r	1,194+02
50	8	1,5	417	18	R65922	Human corticotropin r	1,194+02
51	8	1,5	418	17	R97294	Mouae CRP RAl recepto	1,194+02
52	9	1,5	431	15	R09575	Rat CRP2-beta recepto	1,194+02
53	9	1,5	431	15	R97293	Mouae CRP RAl recepto	1,194+02
54	7	1,3	76	12	R58653	Human CRP RAl recepto	1,192+01
55	7	1,3	393	8	R41878	Human glucagon recepto	1,192+01
56	7	1,3	394	8	R50594	Sequence encoded by f	1,192+01
57	7	1,3	395	8	R50595	Sequence encoded by f	1,192+01
58	7	1,3	333	2	R43507	Contract region of fe	1,192+01
59	7	1,3	333	2	R43507	Contract region of fe	1,192+01
60	7	1,3	395	13	R63017	Insect diuretic hormo	1,192+01
61	7	1,3	426	13	R76159	Xanthomonas L-glutamy	1,192+01
62	7	1,3	461	3	R15350	Usp45 protein, 198pgs	1,192+01
63	7	1,3	562	35	R35155	Mercuric ion reductas	1,192+01
64	7	1,3	564	35	R35153	Mercuric ion reductas	1,192+01
65	7	1,3	564	35	R35154	Mercuric ion reductas	1,192+01
66	7	1,3	564	35	R35154	Mercuric ion reductas	1,192+01
67	7	1,3	564	35	R35157	Mercuric ion reductas	1,192+01
68	7	1,3	565	33	R07092	Rat CM1 protein kina	1,192+01
69	7	1,3	602	10	R57050	Neurotrophin factor (1,192+01
70	7	1,3	602	10	R57050	Neurotrophin factor (1,192+01
71	7	1,3	802	20	W06558	Shiketen neurotrophin	1,192+01
72	7	1,3	826	30	W06557	Human hypoxia inducib	1,192+01
73	6	1,1	10	5	R27115	PRN/PRNP receptor fr	1,192+02
74	6	1,1	10	5	R27116	PRN/PRNP receptor fr	1,192+02
75	6	1,1	11	5	R27116	PRN/PRNP receptor fr	1,192+02
76	6	1,1	11	13	R70440	Ca ²⁺ calctonin and op	1,192+02
77	6	1,1	11	6	R31396	Tocopherol cyclase fr	1,192+02
78	6	1,1	12	3	W00664	Phosphine-containing	1,192+02
79	6	1,1	12	3	W00664	Phosphine-containing	1,192+02
80	6	1,1	215	15	R78931	HNW specific cytotoxi	1,192+02
81	6	1,1	26	33	W07473	Genetic information	1,192+02
82	6	1,1	28	35	W15086	Peptide monomer used	1,192+02
83	6	1,1	30	35	W15086	Peptide monomer used	1,192+02
84	6	1,1	30	35	W15086	Peptide monomer used	1,192+02
85	6	1,1	36	38	W46114	Predicted antigenic T	1,192+02
86	6	1,1	36	38	R79291	Antigenic Tbp1 peptid	1,192+02
87	6	1,1	56	20	W01867	Serine protease PRSP2	1,192+02
88	6	1,1	56	20	W01867	Serine protease PRSP2	1,192+02
89	6	1,1	91	32	W23632	H. pylori protein, 19	1,192+02
90	6	1,1	95	29	W53322	H. pylori Gp70p110	1,192+02
91	6	1,1	95	22	W20754	H. pylori protein, 19	1,192+02
92	6	1,1	109	18	R90151	Thioredoxin componen	1,192+02
93	6	1,1	109	18	R90151	Thioredoxin componen	1,192+02
94	6	1,1	127	18	R90156	Soft wheat thiorodoxi	1,192+02
95	6	1,1	130	18	R90157	Hard wheat thiorodoxi	1,192+02
96	6	1,1	141	17	W23630	H. pylori protein, 19	1,192+02
97	6	1,1	141	17	W23630	H. pylori protein, 19	1,192+02
98	6	1,1	149	6	R43375	Prod. of ORG4 of plas	1,192+02

99	6	1.1	156.17	571800	8-oxo-deoxyguanosine	2.49e-02
100	6	1.1	159.27	573120	Streptavidin protein	2.49e-02
101	6	1.1	159.27	573121	Streptavidin protein	2.49e-02
102	6	1.1	162.15	579061	3 hydroxy-beta-ionone	2.49e-02
103	6	1.1	163.15	579061	Kluvereroyaes lactia	2.49e-02
104	6	1.1	163.15	579061	Kluvereroyaes lactia	2.49e-02
105	6	1.1	163.15	579061	Kluvereroyaes lactia	2.49e-02
106	6	1.1	166.19	598131	Neisseria meningitidis	2.49e-02
107	6	1.1	166.19	598131	Neisseria meningitidis	2.49e-02
108	6	1.1	211.29	555334	H. pylori ORF 07ap110	2.49e-02
109	6	1.1	211.29	555334	H. pylori ORF 07ap110	2.49e-02
110	6	1.1	211.29	555334	H. pylori ORF 07ap110	2.49e-02
111	6	1.1	211.29	555334	H. pylori ORF 07ap110	2.49e-02
112	6	1.1	224.9	584596	fbp2, for reverse gen	2.49e-02
113	6	1.1	224.9	584596	fbp2, for reverse gen	2.49e-02
114	6	1.1	230.17	593144	The DNA polymerase C-	2.49e-02
115	6	1.1	230.17	593144	The DNA polymerase C-	2.49e-02
116	6	1.1	230.17	593144	The DNA polymerase C-	2.49e-02
117	6	1.1	230.17	593144	The DNA polymerase C-	2.49e-02
118	6	1.1	255.23	707850	Dalys-endothelin	2.49e-02
119	6	1.1	255.23	707850	Dalys-endothelin	2.49e-02
120	6	1.1	265.12	871956	P820175 10 kDa toxin.	2.49e-02
121	6	1.1	265.12	871956	P820175 10 kDa toxin.	2.49e-02
122	6	1.1	265.12	871956	P820175 10 kDa toxin.	2.49e-02
123	6	1.1	265.12	871956	P820175 10 kDa toxin.	2.49e-02
124	6	1.1	345.19	848749	G-protein coupled hum	2.49e-02
125	6	1.1	345.19	848749	G-protein coupled hum	2.49e-02
126	6	1.1	345.19	848749	G-protein coupled hum	2.49e-02
127	6	1.1	345.19	848749	G-protein coupled hum	2.49e-02
128	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
129	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
130	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
131	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
132	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
133	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
134	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
135	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
136	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
137	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
138	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
139	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
140	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
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144	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
145	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
146	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
147	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
148	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
149	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02
150	6	1.1	372.29	940135	Rat Gal2 receptor, pr	2.49e-02

RESULT	5	
ID	R27705 standard; Protein: 585 AA.	
AC	R27705:	
DT	16-MAR-1993 (first entry)	
DE	Opesum kidney PH/PPRP receptor prod. from clone ON-O.	
DD	Partlyfold hormone; related protein; calcium; antagonist;	
PM	Partlyfold hormone; related protein; calcium; antagonist;	
OS	Bideltopsis virginiana	

KW Parathyroid Hormone-related protein; calcium: antagonist;
KX hypercalcaemia.
LA Idiopathic hypocalcaemia.
LB Idiopathic hypocalcaemia.
LC W09217602-A.
LD 15-OCT-1992.
LE 06-APR-1992; 028281.
LF 06-APR-1992; 028281.
LG 06-APR-1992; US-864475.
LH (GENO) GEN HOSPITALI CORP OFFICE TECHNOLOGY.
LI Aboon-tamr A, Juppner H, Kronenberg HM, Potts JT, Scilipani E;
PJ Segre GV; 045271/A.
PK N-PGDB: Q36605.
PL N-PGDB: Q36605.
PM New DNA encoding parathyroid hormone receptor, cDNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PP and treatment of tumours English
PR The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
PS receptor protein sequence was deduced from the cDNA sequence of the
CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
CC is identical to the OK-H clone except at the C-terminal tail as OK-O
CC encodes three amino acids, Glycine, Glutamic acid, and Serine. These
CC three differences attributable to the presence of a stop codon in the
CC sequence causing a frame shift and an earlier stop codon. It is not
CC known whether OK-O and OK-H represent prods. of two separate genes or
CC a laboratory artifact. The protein may be used in a therapeutic
CC compen. to inhibit activation of PTH or PTHrP and thus reduce the
CC release of calcium from bone. The protein may also be used with PTH
CC or PTHrP for binding can be identified using the protein prod. and
CC DNAs homologous to PTH DNA can be identified using fragments of the
CC clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC disorders related to the interaction between calcitonin receptor and a
CC protein called hypercalcaemia. See also K177041-1.
CC Sequence: 585 AA;
SQ

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Query Match      4.68; Score 25; DB 5; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.10e-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      207 gyfrrhctnryibmhifvsfalra 231
      |||
QV      167 GYPRRLKTRNYINMHLFVSFALRA 191

```

Page 28

CC	secretin receptor protein encoded by this gene may be used in basic research and clinical tests, and is available in high yield.
CC	
CC	
SQ	Sequence 449 AA:
	Query Match 3 54 Score 19 DB 6 Length 449:
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011

in the blood. Cpds. capable of competing with PTH or PTHrP for binding can be identified using the protein and DNA homologous to PTH DNA can be identified using fragments of the clone as probes. The sequence may be used for the prodn. of antibodies useful for the treatment, classification, prognosis and/or treatment of disorders related to the interaction between a cell receptor and a ligand such as in hypercalcaemia. See also 827704-16.

Query Match 3.34; Score 18; DB 5; Length 591;
Best Local Similarity 100.0%; Pred. No. 2,906-15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 yf1atnywlvilveglylh 307
QY 245 YFLATNYWLVILVEGLYLN 262

RESULT

ID R92277 standard; Protein: 591 AA.
DC 18-MAY-1996 (first entry)
DE Rat bone PTH/PTHrP receptor.
KW Parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
OS Hypercalcaemia; cancer.
RH Rattus sp.
PH Key Location/Qualifiers
FT region 1..192
FT /label= Extracellular_region
FT region 193..211
FT /label= Transmembrane_region
FT region 212..221
FT /label= Intracellular_region
FT region 222..244
FT /label= Transmembrane_region
FT region 245..299
FT /label= Extracellular_region
FT region 300..316
FT /label= Transmembrane_region
FT region 317..326
FT /label= Intracellular_region
FT region 326..342
FT /label= Transmembrane_region
FT region 343..353
FT /label= Extracellular_region
FT region 354..383
FT /label= Transmembrane_region
FT region 384..408
FT /label= Intracellular_region
FT region 409..428
FT /label= Transmembrane_region
FT region 429..444
FT /label= Intracellular_region
FT region 445..464
FT /label= Transmembrane_region
FT region 464..591
FT /label= Intracellular_region
PN US5494806-A.

PI Schipani E, Segre GV;
DR WPI: 96-139028/14.
DR DNA encoding vertebrate parathyroid hormone receptor - useful for
PI cancer etc.
PI Claim 1: Fig 6A-6G: 64pp; English.
CC A human parathyroid hormone/parathyroid hormone-related protein
CC (PTH/PTHrP) receptor (R92278) is encoded by cDNA clone HK-1.
CC This receptor is a G-protein coupled receptor which induces an
CC increase in intracellular cAMP and intracellular free
CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
CC be produced in vector/host cell systems and used in the treatment,
CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
CC screen for (ant)agonists and to raise antibodies. Host cells
CC expressing the receptor are used for diagnostic measurement of PTH
CC or PTH serum levels. See also R27704-16.

Query Match

Best Local Similarity 100.0%; Pred. No. 2,906-15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 yf1atnywlvilveglylh 307
QY 245 YFLATNYWLVILVEGLYLN 262

RESULT

ID R27707 standard; Protein: 614 AA.
AC R27707.
DT 16-MAR-1993 (first entry)
DE Rat bone PTH/PTHrP receptor.
KW Parathyroid hormone-related protein; calcium; antagonist;
OS Synthetic.
OS Homo sapiens.
PH 15-OCT-1992.
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
DR WPI: 92-36627/44.
DR New DNA encoding parathyroid hormone receptor, DNA and antibodies
DR for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
PT Claim 22: Fig 6: 91pp; English.
CC The protein sequence was deduced from the cDNA sequence obt'd by

PI Schipani E, Segre GV;
DR WPI: 96-139028/14.
DR DNA encoding vertebrate parathyroid hormone receptor - useful for
PI diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PI cancer etc.
PI Claim 1: Fig 3A-3F: 64pp; English.
CC A human parathyroid hormone-related protein
CC (PTH/PTHrP) receptor (R92277) is encoded by cDNA clone HK-1.
CC This receptor is a G-protein coupled receptor which induces an
CC increase in intracellular cAMP and intracellular free
CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
CC be produced in vector/host cell systems and used in the treatment,
CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
CC screen for (ant)agonists and to raise antibodies. Host cells
CC expressing the receptor are used for diagnostic measurement of PTH
CC or PTH serum levels. See also R27704-16.

Query Match

Best Local Similarity 100.0%; Pred. No. 2,906-15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 yf1atnywlvilveglylh 307
QY 245 YFLATNYWLVILVEGLYLN 262

RESULT

ID R92278 standard; Protein: 593 AA.
DC 18-MAY-1996 (first entry)
DE Human kidney PTH/PTHrP receptor.
KW Parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
OS Homo sapiens.
PH 15-OCT-1992.
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
DR WPI: 92-36627/44.
DR New DNA encoding parathyroid hormone receptor, DNA and antibodies
DR for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
PT Claim 25: Page 5: 91pp; English.
CC The peptide sequence shown represents an extracellular fragment of
CC the PTH/PTHrP receptor protein. The peptide is capable of binding
CC PTH or PTHrP and acting as an antagonist of these cpds. The
CC peptide may be used to inhibit activation of PTH or PTHrP and thus
CC reduce the level of calcium in the blood. Cpds. capable of competing

PI Schipani E, Segre GV;
DR WPI: 96-139028/14.
DR DNA encoding vertebrate parathyroid hormone receptor - useful for
PI cancer etc.
PI Claim 1: Fig 6A-6G: 64pp; English.
CC A human parathyroid hormone/parathyroid hormone-related protein
CC (PTH/PTHrP) receptor (R92278) is encoded by cDNA clone HK-1.
CC This receptor is a G-protein coupled receptor which induces an
CC increase in intracellular cAMP and intracellular free
CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
CC be produced in vector/host cell systems and used in the treatment,
CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
CC screen for (ant)agonists and to raise antibodies. Host cells
CC expressing the receptor are used for diagnostic measurement of PTH
CC or PTH serum levels. See also R27704-16.

Query Match

Best Local Similarity 100.0%; Pred. No. 2,906-15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 yf1atnywlvilveglylh 307
QY 245 YFLATNYWLVILVEGLYLN 262

RESULT

ID R27710 standard; peptide: 19 AA.
AC R27710.
DT 16-MAR-1993 (first entry)
DE Rat bone PTH/PTHrP receptor.
KW Parathyroid hormone-related protein; calcium; antagonist;
OS Synthetic.
OS Homo sapiens.
PH 15-OCT-1992.
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
DR WPI: 92-36627/44.
DR New DNA encoding parathyroid hormone receptor, DNA and antibodies
DR for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
PT Claim 25: Page 5: 91pp; English.
CC The peptide sequence shown represents an extracellular fragment of
CC the PTH/PTHrP receptor protein. The peptide is capable of binding
CC PTH or PTHrP and acting as an antagonist of these cpds. The
CC peptide may be used to inhibit activation of PTH or PTHrP and thus
CC reduce the level of calcium in the blood. Cpds. capable of competing

CC culturing cells transformed by the vector. The peptides can be
CC used to raise antibodies. The peptides and antibodies are useful
CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and
CC hypocalcaemia, and can also be used to screen for (anti)agonists
CC of therapeutic appln.
SQ Sequence 10 AA.

Query Match 1.89; Score 10; DB 16; Length 10;
Best Local Similarity 100.00; Pred. No. 2.81e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 frfihctny 10
QY 169 FRUHCYNY 178
|||||

RESULT 17
ID R57829 standard; Protein: 162 AA.
AC R57829 standard; Protein: 162 AA.
DE Human GR C-terminal (clone 40-2-2).
KW Rat; human; glucagon receptor; transgenic animal; metabolism; model;
RW amplification; primer; polymerase chain reaction; PCR.
PN W09057829.
PP 17-MAR-1994.
PF 30-AUG-1993; 081174.
PR 28-AUG-1993; US-938331.
PS 28-AUG-1993; US-938331.
PT (SINO) SYNTHETICS INC.
PI Foster DC, Grant FJ, Jelinek LJ, Kindavogel WR;
PI Kujiper JL, Lok S, O'Hara PJ, Sheppard PO;
PI N-PSDB: Q67247.
DR N-PSDB: Q67247.
DT New recombinant glucagon receptor and antibodies - useful to
PT produce model transgenic animals for study and with therapeutic
PT applications.
PT Example 5 describes the isolation of human GR.
CC The GR coding sequence was constructed from partial clone
CC p9A11 (5' end) and clone 40-2-2 (3' end).
CC Host cells cony. GR DNA may be used for the prodn. of
CC recombinant GR. GR DNA may also be expressed in non-human
CC transgenic animals, pref. mice. Such animals may be readily
CC used as models to study the role of the glucagon receptor
CC in metabolism.
SQ Sequence 162 AA.

Query Match 1.89; Score 10; DB 10; Length 162;
Best Local Similarity 100.00; Pred. No. 2.81e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW adenylylate cyclase; receptor; type 1A; signal sequence;
KW hydrophobic cluster; transmembrane; pituitary;
KW gland-derived; diagnosis; neuropathy; Alzheimer's disease; gene therapy;
KW screening; assay; neuropathy.
PN S7418531-A.
PP 05-OCT-1994.
PF 24-FEB-1994; 102757.
PR 26-FEB-1993; JP-018755.
PS 26-FEB-1993; JP-018755.
PR 27-APR-1993; JP-100669.
PR 17-MAY-1993; JP-114446.
PR 24-JUN-1993; JP-133963.
PR 24-JUN-1993; JP-133963.
PR 27-DEC-1993; JP-133175.
PR (TAKA) TAKEDA CHEM IND LTD.
PI Nabeta Y, Hosoya M, Ishibashi Y, Kitada C, Masuda Y;
PI Miyamoto Y, Ogi K, Ohtaki T, Onda H, Shimamoto M;
PI New pituitary adenylylate cyclase activating polypeptide receptor
PT treatment of neuropathy such as Alzheimer's disease
PT proteins - used to develop prods. for use in the diagnosis and
PT treatment of neuropathy such as Alzheimer's disease
CC Claim 2, Page 31: 44pp. English (5961-54) describing the regions of high
CC homology between the human, bovine and rat pituitary adenylylate cyclase
CC activating polypeptide (PACAP) receptor proteins. The genes (Q71203-10)
CC encode proteins (R58655-62) of around 500-550 amino acids. The proteins
CC contain a signal sequence which may be cleaved to produce mature proteins
CC (R58663-71). Regions of high homology between the human, bovine and
CC contain 7 hydrophobic clusters considered to be transmembrane domains in
CC tandem. The gene for the bovine PACAP receptor was cloned by purifying
CC the protein to homogeneity. A probe was constructed to match the N-terminal
CC of the protein to homogeneity. A probe was constructed to match the N-terminal
CC of the protein to homogeneity. A probe was constructed to match the N-terminal
CC to obtain a cDNA clone of the PACAP receptor. The DNA sequence was used
CC to obtain human PACAP receptor cDNA from a human pituitary gland-derived
CC cDNA library. The rat PACAP receptor gene was cloned by constructing
CC primers based on the homology between the PACAP receptor and the
CC human PACAP receptor. The rat PACAP receptor gene was cloned by constructing
CC primers based on the homology between the PACAP receptor and the
CC human PACAP receptor. The rat PACAP receptor gene was cloned by constructing
CC fragments thereof may be used for the diagnosis of neuropathy such as
CC Alzheimer's disease. The DNA encoding the PACAP receptor can be used for
CC for treating neuropathy.
SQ Sequence 50 AA.

Query Match 1.74; Score 9; DB 12; Length 50;
Best Local Similarity 100.00; Pred. No. 1.9e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 lveglylhl 108
QY 255 lveglylhl 264
|||||

RESULT 18
ID R50047 standard; Protein: 477 AA.
AC R50047 standard; Protein: 477 AA.
DE Vasoactive intestinal peptide (VIP) 2 receptor.
KW Rat; human; glucagon receptor; transgenic animal; metabolism; model;
RW signal sequence; transmembrane domain; glycosylation site.
PN W95405798A.
PP 30-AUG-1993; 081174.
PR 28-AUG-1992; US-938331.
PS 01-JUL-1993; US-086631.
PT (SINO) SYNTHETICS INC.
PI Foster DC, Grant FJ, Jelinek LJ, Kindavogel WR;
PI Kujiper JL, Lok S, O'Hara PJ, Sheppard PO;
PI N-PSDB: Q59776.
DR N-PSDB: Q59776.
DT New recombinant glucagon receptor and antibodies - useful to
PT produce model transgenic animals for study and with therapeutic
PT applications.
PT Claim 4, Page 91-95; 112pp. English.
PS Rat and human glucagon receptor (GR) DNA was isolated.
CC Rat and human GR DNA may be used for the prodn. of
CC recombinant GR. GR DNA may also be expressed in non-human
CC transgenic animals, pref. mice. Such animals may be readily
CC used as models to study the role of the glucagon receptor
CC in metabolism.
SQ Sequence 477 AA.

Query Match 1.89; Score 10; DB 10; Length 477;
Best Local Similarity 100.00; Pred. No. 2.81e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 243 lveglylhl 252
QY 255 lveglylhl 264
|||||

RESULT 19
ID R58649 standard; Peptide: 50 AA.
AC R58649 standard; Peptide: 50 AA.
DE PACAP receptor protein homology region 7.
KW Bovine; pituitary adenylylate cyclase activating polypeptide; PACAP;

QY 183 lveglylhl 191

RESULT 20
ID R70136 standard; Protein: 437 AA.
AC R70136 standard; Protein: 437 AA.
DE Vasoactive intestinal peptide (VIP) 2 receptor.
KW Rat; human; glucagon receptor; transgenic animal; metabolism; model;
RW signal sequence; transmembrane domain; glycosylation site.
PN W95405798A.
PP 30-AUG-1993; 081174.
PR 28-AUG-1992; US-938331.
PS 01-JUL-1993; US-086631.
PT (SINO) SYNTHETICS INC.
PI Foster DC, Grant FJ, Jelinek LJ, Kindavogel WR;
PI Kujiper JL, Lok S, O'Hara PJ, Sheppard PO;
PI N-PSDB: Q59776.
DR N-PSDB: Q59776.
DT New recombinant glucagon receptor and antibodies - useful to
PT produce model transgenic animals for study and with therapeutic
PT applications.
PT Claim 4, Page 91-95; 112pp. English.
PS Rat and human glucagon receptor (GR) DNA was isolated.
CC Rat and human GR DNA may be used for the prodn. of
CC recombinant GR. GR DNA may also be expressed in non-human
CC transgenic animals, pref. mice. Such animals may be readily
CC used as models to study the role of the glucagon receptor
CC in metabolism.
SQ Sequence 477 AA.

Query Match 1.89; Score 10; DB 10; Length 477;
Best Local Similarity 100.00; Pred. No. 2.81e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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Query Match      1.7%  Score 9; DB 12; Length 448;
Best-Local Similarity 100.0%; Pred. No. 6.5e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 172 ltvasfmlra 180
| | | | | | | |
QY 183 ltvafslmlra 191
| | | | | | | |

RESULT 24 standard. Database: 453 kb
RESULT 70026

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MC R300/L;
DT 12-MAY-1995 (first entry)

alternative splicing of a transcription product from a common gene. The PACAP receptor or fragments thereof may be used for the diagnosis of

:

12-MAY-1995 (first entry)

CC PACAP receptor or fragments thereof may be used for the diagnosis of
CC neuropathy such as Alzheimer's disease. The DNA encoding the PACAP

RESULT	42
ID	M1681 standard; Protein: 411 AA.
AC	M1681:
DC	Human corticotropin releasing factor 2 receptor protein.
DE	Human corticotropin releasing factor 2 receptor protein. Csp2.
EN	receptor; screen; agonist; antagonist; activation; inhibition;
KW	stress adaptation; dementia; obesity; acceleration;
PM	protection; treatment; melancholia; anxiety stress headache; AIDS;
RN	screen immunodeficiency syndrome; Alzheimer's disease;
RS	Homo sapiens.
SD	J09070289-A.
PD	18-MAR-1997.
PP	27081.
PF	14-SEP-1995.
PI	27081, 3
PA	(NAME) TAKEDA CHEMIND LTD.

Page 68

	RESULT	43	RN0576 standard; Protein: 411 AA.
ID	AC	RN0576	1996 (first entry)
DE	DE	Human CRP2 receptor	
DE	DE	CRP2 receptor; corticotropin-releasing factor-3 receptor;	
NM	NM	cerebrovascular disorder; memory disorder; Alzheimer disease.	
NC	NC	K09344651.A2	
PD	PD	21-DEC-1995.	
PF	PF	14-JUN-1995:	D07753
PF	PF	11-MAY-1995:	D07859
PF	PF	31-JAN-1995:	US-781433
PF	PF	07-JUN-1995:	US-483984
PA	PA	(NEUR.) NEUROSCIENCE SCIENCES INC.	
PI	PI	Leobenweg 79, Oldensdorf Tl,	
PI	PI	MPI-95-045680/Q5.	
DR	DR	K-PUBS: 1124747	
DR	DR	used to isolate CRP2 receptor antagonists for the treatment of	
PT	PT	cerebrovascular disorders, memory disorders and Alzheimer's disease	
PT	PT	Disclosure: Page 80-82; 10ppg English.	
CC	CC	membrane-bound G-coupled protein receptor; translation of encoding cDNA	
CC	CC	transduction. It can be produced by expression of encoding cDNA	

DB	349 atgagttta 356
QY	403 sfoqpfvts 410

RESULT 44

ID R00574 standard; Protein: 411 AA.

AC R00574:

DT 08-APR-1996 (first entry)

DE Cys α_2 -alpha receptor-ticotropin-releasing factor-2 receptor;

KW carbovascular disorder; memory disorder; Alzheimer disease;

Ft		domain	/label= Extracellular_N-terminal_domain
Ft	7-119	domain	
Ft	118-136	domain	/label= Transmembrane_Domain
Ft		domain	
Ft	139-147	domain	/label= Intracellular_domain
Ft	148-167	domain	/label= Transmembrane_Domain
Ft		domain	
Ft	168-184	domain	/label= Extracellular_domain
Ft	185-208	domain	/label= Transmembrane_Domain
Ft		domain	
Ft	209-223	domain	/label= Intracellular_domain
Ft	224-244	domain	/label= Transmembrane_Domain
Ft		domain	
Ft	245-261	domain	/label= Extracellular_domain
Ft	262-286	domain	/label= Transmembrane_Domain
Ft		domain	
Ft	287-309	domain	/label= Intracellular_domain
Ft	310-329	domain	/label= Transmembrane_Domain
Ft		domain	
Ft	330-342	domain	/label= Extracellular_domain
Ft	343-363	domain	

FT	domain	/Label: Transmembrane_domain
FT		364..411
FT		/Label: C-terminal_intracellular_domain
PP	21	NP055461.1.2.
PP	24	NP055461.2.
PP	24	NP055461.3.
PP	14	JUN-1995: U07757.
PP	14	JUN-1995: U8-25999.
PP	14	JUN-1995: U8-25999.
PP	01	JUN-1995: U8-265931.
PP	01	JUN-1995: U8-265931.
PA	(NEUR.) NEUROSCIENCE SCIENCES INC.	
PA	Chalmers D., De Souza MB., Grigoriadis DE., Liaw CW;	
PPI	January 27, 1995	
PPI	University of Oldenburg T.	
PPI	NP05281.1.2.	
PPI	NP05281.2.	
PP	NP05281.3.	
PP	NP05281.4.	
PP	NP05281.5.	
PP	NP05281.6.	
PP	NP05281.7.	
PP	NP05281.8.	
PP	NP05281.9.	
PP	NP05281.10.	
PP	NP05281.11.	
PP	NP05281.12.	
PP	NP05281.13.	
PP	NP05281.14.	
PP	NP05281.15.	
PP	NP05281.16.	
PP	NP05281.17.	
PP	NP05281.18.	
PP	NP05281.19.	
PP	NP05281.20.	
PP	NP05281.21.	
PP	NP05281.22.	
PP	NP05281.23.	
PP	NP05281.24.	
PP	NP05281.25.	
PP	NP05281.26.	
PP	NP05281.27.	
PP	NP05281.28.	
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PP	NP05281.30.	
PP	NP05281.31.	
PP	NP05281.32.	
PP	NP05281.33.	
PP	NP05281.34.	
PP	NP05281.35.	
PP	NP05281.36.	
PP	NP05281.37.	
PP	NP05281.38.	
PP	NP05281.39.	
PP	NP05281.40.	
PP	NP05281.41.	
PP	NP05281.42.	
PP	NP05281.43.	
PP	NP05281.44.	
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PP	NP05281.62.	
PP	NP05281.63.	
PP	NP05281.64.	
PP	NP05281.65.	
PP	NP05281.66.	
PP	NP05281.67.	
PP	NP05281.68.	
PP	NP05281.69.	
PP	NP05281.70.	
PP	NP05281.71.	
PP	NP05281.72.	
PP	NP05281.73.	
PP	NP05281.74.	
PP	NP05281.75.	
PP	NP05281.76.	
PP	NP05281.77.	
PP	NP05281.78.	
PP	NP05281.79.	
PP	NP05281.80.	
PP	NP05281.81.	
PP	NP05281.82.	
PP	NP05281.83.	
PP	NP05281.84.	
PP	NP05281.85.	
PP	NP05281.86.	
PP	NP05281.87.	
PP	NP05281.88.	
PP	NP05281.89.	
PP	NP05281.90.	
PP	NP05281.91.	
PP	NP05281.92.	
PP	NP05281.93.	
PP	NP05281.94.	
PP	NP05281.95.	
PP	NP05281.96.	
PP	NP05281.97.	
PP	NP05281.98.	
PP	NP05281.99.	
PP	NP05281.100.	
PP	NP05281.101.	
PP	NP05281.102.	
PP	NP05281.103.	
PP	NP05281.104.	
PP	NP05281.105.	
PP	NP05281.106.	
PP	NP05281.107.	
PP	NP05281.108.	
PP	NP05281.109.	
PP	NP05281.110.	
PP	NP05281.111.	
PP	NP05281.112.	
PP	NP05281.113.	
PP	NP05281.114.	
PP	NP05281.115.	
PP	NP05281.116.	
PP	NP05281.117.	
PP	NP05281.118.	
PP	NP05281.119.	
PP	NP05281.120.	
PP	NP05281.121.	
PP	NP05281.122.	
PP	NP05281.123.	
PP	NP05	

```

Query Match      1.59:  Score 8; DB 15; Length 411;
Best Local Similarity 100.0%;  Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Db      349  agcggfva 356
QY      403  sfocgfvs 410

```

	45	RESULT
ID	R9730 standard: Protein: 415 AA.	
AC	R9730, 1996 (f1est entry)	
DE	Human GTP-binding protein	
DE	Human GTP receptor GTP-R1	
DE	Corticotropin releasing factor receptor: CRF-R: corticoliberin:	
RW	signal transduction.	
OS	Momo sapiens.	
FT	Location/Qualifiers	
FT	modified_site 38	
FT	/label: N-glycosylation:site	
FT	modified_site 45	
FT	/label: N-glycosylation:site	
FT	modified_site 46	
FT	/label: N-glycosylation:site	
FT	modified_site 47	
FT	/label: N-glycosylation:site	

Nov 24 06:10:58 1998

US-08-461-011A-2.rag

Db 353 pfqgrfva 360
Qy 403 pfqgrfva 410

REUT	46
ID:	R9732 standard; Protein. 415 AA.
AC	R9732:
DT	21-AUG-1986 (first entry)
PT	CDR-R: corticotropin-releasing factor receptor: CRP-R: corticocorticeberlin:
KW	signal transduction.
OS	Rattus sp.
ON	Rattus norvegicus.
PD	13-JUN-1986.
PP	06-DEC-1995: U15909.
PR	08-DIC-1994: US-355337.
PX	08-DIC-1994: US-355337.
SA	(SAR) - SARIS IMMUNOLOGICAL STUDIES
PI	Chen R, Boudreau CJ, Lewis KA, Perrin MH, Savchenko P;
PT	Vale WW.
DR	WPI: 86-28179/29.
PT	Isolated corticotropin-releasing factor receptor (CRF-R) - used to
PT	develop prods. for modulating signal transduction activity mediated
PT	by CRF-R.
CC	A new G-protein-coupled protein, CRP-R (897292), has high
CC	binding affinity for corticotropin releasing factor (CRF). The
CC	amino acid sequence was deduced from a cDNA clone (Tg9970) isolated
CC	from a rat brain cDNA library. This cDNA can be used for prodn. of
CC	antagonists that modulate the signal transduction activity mediated
CC	by CRF receptors. It can be administered therapeutically to
CC	reduce high ACTH levels caused by excess CRF.

```

Query Match      1 st      Score 8   DB 17, Length 415:
Best Local Similarity 100.0%
Accession No. 1914400
Matches 8: Conservative      0; Indels 0; Gaps 0;
Mismatches 0;
Do 353 sfocgfwps 360
|||||||
Oy 403 sfocgfwps 410

RESULT 47
ID R6919 standard: Protein: 415 AA.
DT 21-AUG-1995 (first entry)

```

[illegible]

Query Match 1.50; Score 8; DB 17; Length 415;
Best Local Similarity 100.00; Pred. No. 1.19e+00;
Matches 8; Consensative 0; Mismatches 0; Indels 0; Cons

DE Human pituitary corticotropin releasing factor receptor CRF-RAL
KW Pituitary; hormone; corticotropin releasing factor receptor;
KW hypothalamus; adrenocorticotrophic hormone; ACTH; Cushing's disease;
KW Cushing's disease

Key	Location/Qualifiers
FT	modified_ssite 38 /notes/ 'glycosylation site'
FT	modified_ssite 45 /notes/ 'glycosylation site'
FT	modified_ssite 78 /notes/ 'glycosylation site'
FT	modified_ssite 90 /notes/ 'glycosylation site'
FT	modified_ssite 98 /notes/ 'glycosylation site'
FT	modified_ssite 146 /notes/ 'glycosylation site'
FT	modified_ssite 222 /notes/ 'protein-kinase-C phosphorylation site'
FT	modified_ssite 396 /notes/ 'protein-kinase-C phosphorylation site'
FT	modified_ssite 408 /notes/ 'protein-kinase-C phosphorylation site'
FT	modified_ssite 498 /notes/ 'protein-kinase-C phosphorylation site'
FT	modified_ssite 502 /notes/ 'casein-kinase-II phosphorylation site'
FT	modified_ssite 302 /notes/ 'protein-kinase-A phosphorylation site'
FT	W03500610-A.
PD	05-JAN-1995.
PD	25-MAY-1994.
PD	18-JUN-1993.
PD	08-079320.
PD	08-079320.
PA	(SALK) SALK INST BIOLOGICAL STUDIES
PA	Chen R, Donaldson GJ, Levis KA, Perrin MH, Vale MW;
DI	WPI: 95-03207/07.

[illegible]

AC R69521: 1.5%; Score 8; DB 13; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 48
ID W00159 standard; Protein: 415 AA.
DC W00159: 1996 (first entry)
DE Human corticotropin releasing factor receptor protein.
KW Human; corticotropin releasing factor; CRF receptor;
KW expression vector: pAC02; agonist; antagonist; blood pressure;
OS Homo sapiens.
PN J08140680-A.
PD 04-JUN-1996.
PR 22-NOV-1994: JP-287638.
PA (TAKA) TAKEDA CHEM IND LTD.
DR WPI: 96-31616/32.
DR N-PDB: 170568.
CC This sequence represents human corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 13; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 50
ID R69521 standard; Protein: 415 AA.
DC R69521: 1996 (first entry)
DE Mouse CRF RAL receptor.
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
OS Mus sp.
PN Mus sp.
PD 21-AUG-1996.
PR 21-AUG-1996: (first entry)
PA Corticotropin releasing factor receptor; CRF-R; corticoliberin;
DR WPI: 95-053077/07.
DR N-PDB: Q81954.
CC This sequence represents mouse corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 13; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 48
ID W00159 standard; Protein: 415 AA.
DC W00159: 1996 (first entry)
DE Human corticotropin releasing factor receptor protein.
KW Human; corticotropin releasing factor; CRF receptor;
KW expression vector: pAC02; agonist; antagonist; blood pressure;
OS Homo sapiens.
PN J08140680-A.
PD 04-JUN-1996.
PR 22-NOV-1994: JP-287638.
PA (TAKA) TAKEDA CHEM IND LTD.
DR WPI: 96-31616/32.
DR N-PDB: 170568.
CC This sequence represents human corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 18; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 49
ID R69521 standard; Protein: 415 AA.
DC R69521: 1996 (first entry)
DE Mouse CRF RAL receptor.
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
OS Mus sp.
PN Mus sp.
PD 21-AUG-1996.
PR 21-AUG-1996: (first entry)
PA Corticotropin releasing factor receptor; CRF-R; corticoliberin;
DR WPI: 95-053077/07.
DR N-PDB: Q81954.
CC This sequence represents mouse corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 13; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 50
ID R69521 standard; Protein: 415 AA.
DC R69521: 1996 (first entry)
DE Mouse CRF RAL receptor.
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
OS Mus sp.
PN Mus sp.
PD 21-AUG-1996.
PR 21-AUG-1996: (first entry)
PA Corticotropin releasing factor receptor; CRF-R; corticoliberin;
DR WPI: 95-053077/07.
DR N-PDB: Q81954.
CC This sequence represents mouse corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 17; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 49
ID R69521 standard; Protein: 415 AA.
DC R69521: 1996 (first entry)
DE Mouse CRF RAL receptor.
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
OS Mus sp.
PN Mus sp.
PD 21-AUG-1996.
PR 21-AUG-1996: (first entry)
PA Corticotropin releasing factor receptor; CRF-R; corticoliberin;
DR WPI: 95-053077/07.
DR N-PDB: Q81954.
CC This sequence represents mouse corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 18; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 49
ID R69521 standard; Protein: 415 AA.
DC R69521: 1996 (first entry)
DE Mouse CRF RAL receptor.
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
OS Mus sp.
PN Mus sp.
PD 21-AUG-1996.
PR 21-AUG-1996: (first entry)
PA Corticotropin releasing factor receptor; CRF-R; corticoliberin;
DR WPI: 95-053077/07.
DR N-PDB: Q81954.
CC This sequence represents mouse corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.

Query Match 1.5%; Score 8; DB 17; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.19e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 353 sfqgfsvs 360
QY 403 sfqgfsvs 410

RESULT 49
ID R69521 standard; Protein: 415 AA.
DC R69521: 1996 (first entry)
DE Mouse CRF RAL receptor.
KW Corticotropin releasing factor receptor; CRF-R; corticoliberin;
OS Mus sp.
PN Mus sp.
PD 21-AUG-1996.
PR 21-AUG-1996: (first entry)
PA Corticotropin releasing factor receptor; CRF-R; corticoliberin;
DR WPI: 95-053077/07.
DR N-PDB: Q81954.
CC This sequence represents mouse corticotropin releasing factor (CRF) receptor designated pAC02. pAC02 is an expression vector constructed for elevated expression of the human CRF receptor protein. The recombinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist. The agonist and antagonist may be used for the treatment of blood pressure, and antagonists may be used for the treatment of immunosuppression.




```

US-08-468-011A-1.rpt
Title Nov 24 09:10:59 1998

Trace covered overall poor quality
Seq primer: -40ml fvd. ET from Amrham
High quality sequence stop: 1.
Location/Qualifiers
    /organism=Homo sapiens*
    /method=PCR
    /modified=polylinker; site_1_Not 1; site_2:
        normal
        Normal amounts of plasmid DNA from three normal
        individuals were digested with EcoRI and
        NciI/GAP CGcl) were mixed, and as circles were
        ligated. Following HAP purification, this DNA was
        tracer in a subtractive hybridization reaction
        from the spleen T lymphocytes from pool(s) of 5,000
        clones. The subtracted DNA was digested with
        I.M.A.G.E. clones 278480-102087, 682632-687239,
        726408-728711, and 728096-731398. Subtraction
        Soares and M. Fatima Bonaldo.*
        /clone_id=I.M.A.G.E.168891
        /clone_lib=Soares NFL T GBC S1*
        /lab_host=DH10B
BASE COUNT      143 a 136 c 127 g   146 t
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

Db 459 GGCGCTGCCGAGGGCAG 478
Cp 162 GGCGCTGCCGAGGGCAG 143

RESULT 5
LOCUS       FR00061330          618 bp      DNA
DEFINITION  R-buripes GSS sequence, clone 106C21ba2, genomic survey
ACCESSION  Z89940
VERSION    02567134
KEYWORDS   Genomic survey sequence.
SOURCE     Fugu buripes
ORGANISM   Fugu buripes
            Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata
            Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Tetraodontiformes; Tetraodon; Tetraodontidae; Fugu
            1 (bases 1 to 618)
AUTHORS    Exig,G., Clark,M., Smith,S., Meek,S., Warner,S., Umran
            Williams,G. and Brenner,S.
TITLE      Submitted (18-FEB-1997) WRC Human Genome Mapping Project
JOURNAL

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```

US-08-468-031A-1.1.rpt

Tue Nov 24 09:10:58 1998

Clone was randomly picked from subtracted KGLa primary
library.
Seq primer: 5' GAATTAACCTCACTAAAGG 3'
High quality sequence stop: 220.
100% Homology/Qualifiers
1 220
/organism=Homo sapiens
/notes=Vector: Lambda Zap Express (Stratagene)
EcoRI; Site.2: XhoI; Unidirectional cloning site
XhoI-XbaI; mMuV was purified from AG12 cell
library. The library was digested with XbaI and
adaptors were ligated, followed by digestion by
XhoI. The library was then digested with XbaI and
directional cloning into predigested Lambda Zap
/ab_xref=taxon:9606
/clone_lib=KGLa; Lambda Zap Express cDNA library
/contig=KGLa; contig
/cell_line=KGLa
30 a 54 c 86 g 48 t

BASE COUNT
ORIGIN
Query Match 0.94; Score 19; DB 18; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0;

Db 43 TGGCGTCGTCGTCGTCGCG 61
|||||
Cp 1474 TGGCTGCTGCTGCTGTCGCG 1456

7 AA342311 225 bp mRNA EST 21-APR-98
DEFINITION ESF747875 Fetal spleen Homo sapiens cDNA 3' end, mRNA sequence
AA342311
NCBI 91994609
FEATURES
ORIGIN
ORGANISM
Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini;
Homo
Homo bases 1 to 235)
Adams M.D., Soares M.B., Kerlavage,A.R., Fields,C. and
Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
Nucleic Acids Res. 21, 373-380 (1993)
Other ESTs: ES747876
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
University of Maryland, Baltimore, MD 20850, USA
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```


Tue Nov 24 08:10:58 1998

[illegible]

```

email: Location/Qualifiers n.
FEATURES
    source
        1..241
            /cld="Homo sapiens"
            /cldm="A1472"
            /cldm="53 c"
BASE COUNT      50 a      91 g      47 t
ORIGIN
Query Match      0.9%
Best Local Similarity 100.0%
RefSeq No. 1:00e-03;
RefSeq No. 2: conservative
Indels 0; Gaps 0;
DB 51 GTGGCAGGAGGAGCCTC 68
CP 157 GTGGCAGGAGGAGCCTC 140

```

RESULT	17	W40862	249 bp	mRNA	EST	20-MAY-1996
LOCUS		W40862				
DEFINITION		clone 353450 r1 Soares mouse embryo YEM213.5 1.5 Nus musculus cDNA				
ACCESSION		W40862				
NID		9132179				

Tue Nov 24 08:10:58 1998

```

ORIGIN
      10  TTTTCACTCTGCTGAA  27
      1365 TTTTCACTCTGCTGAA  1348
      Cp
      Db
      Best Match          0.9%   Score 18; DB 22; Length 249;
      Query Similarity 100.0%; Pred. No. 1.0e-03;
      Best Local Similarity 100.0%; Pred. No. 1.0e-03;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

Contact: Maria M/Mouse EST Project
 WashU-HMZ Mouse EST Project
 Department of Medicine
 4444 Forest Park Parkway, Box 8001, St. Louis, MO 63108
 Tel: 314 286 1800
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty free through LINC : contact the
 LINC Consortium (informatio.linc.gov) for further information.
 Seq primer: -28m3 rev1 ET from Amerham
 High quality sequence spot: 86.
 Location/Qualifiers
 1. 250
 /organism="Mus musculus"
 /species="MUS"
 /notes="Vector: plasmidscript SK-; Site.1: c2081; Site.2:
 XhoI: HindIII undirectional. Primer: 01502 of 93
 pooled MH/Swiss 13 day embryo hearts. Average insert

Tue Nov 24 08:10:58 1998

```
size: 1.0 kb, Uni-ZAP XR Vector; -5' adaptor sequence: 5'-  
ATGTCGACCGCAGCTGGTCCGTTTG-3';  
+3' adaptor sequence: 3'-  
CTGAGGTGTTTTTTTATTGTTT-3'.  
/db_xref=taxon:10090/  
/clone_id=588352/  
/clemm_lib=Stratagene mouse heart (#37316).  
/embryo_age=P0/  
/dev_stage=E11 day embryos/  
/lab_host=SOLR (kanamycin resistant)
```

ORIGIN	87 A	88 C	70 G	45 T
Query Match	0.94	Score 18	DB 26	Length 250
Best Local Similarity	100.00	Pred. No.	1.03e-03	
Db	93	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
Db	93	CCGACGAGGAGTGAGC	110	
CP	1253	CCGACGAGGAGTGAGG	1236	
RESULT	14			
LOCUS	AA012823	273 bp	nrna	EST
DEFINITION	ze7h04.al	Sortes retina N2b-RR	Homo sapiens	cdna clone 360247 3',
ACCION	AA012823	Sequence.		
NID	91473975			
KEYWORDS				EST.
SOURCE	human			
SOURCEVIEW				

REFERENCE
1. (bases 1 to 273)
Miller, L., Clark, R., Dubuque, T., Ellston, K., Hawkins, M.,
Parsons, J., Rikht, R., Robling, T., Scott, L., Seymour, A., F.,
Trevaaks, E., Waterson, R., Williamson, A., Mohlmann, P. and
Wilson, R.
Vertebrata: Eutheria: Primates: Catarrhini: Homidae; Homo.
Unpublished (1995)

TITLE
The Washo-Merck EST Project

JOURNAL
COMMENT

Contact: Wilson RK
Washo-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: wu@wustl.edu
This clone is available royalty-free through LIGM; contact the
IMAGE Consortium (info@image.llnwd.net) for further information.


```

Query Match      0.93; Score 19; DB 4; Length 297;
Best Local Similarity 90.59; Pred.No. 1.74e-05;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB      228 CACTGCGCTGGGCTGGGAGAT 248
      |||| |||| |||||
QY      1247 CACTGGCGCTGGGCTGGGAGAT 1267

```

RESULT	18	EST	21-APR-1997
LOCUS	A4353845	300 bp	mRNA
DEFINITION	EST2296 Jurkat T-cells V Homo sapiens CDNA 5' end, mRNA sequence.		
ACCION	U0060402		
NID	92066402		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
Eukaryotes:	mitochondrial eukaryotes; Metazoa; Chordata;		
Vertebrate:	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;		

REFERENCE
ACTIONS
 Adams (cases 1 to 300)
 Adams, J., Mayne, A.R., Fietischmann, B.D., Fuldner, R.H.,
 Lee, J., Kuo, H.H., Kirschner, G.P., Weinrobo, C., Govey, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fithgum, W.M., Friedman, J.L., Geoghagen, N.S.,
 Gorman, W., Kell, C.L., Krumholz, C., Redmon, R., Rink, P.S., Jr.,
 Kellon, M., Kellon, M., Kellon, M., Kellon, M., Kellon, M.,
 Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,
 Small, K.V., Spriggs, T.A., Otterback, T.R., Neidman, J.P., Li, Y.,
 Debnar, R., Peng, G., Cepeda, H.M., Coleman, T.A., Collins, E.J.,
 Debnar, R., Peng, G., Cepeda, H.M., Coleman, T.A., Collins, E.J.,
 He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, K.,
 Kozak, D.L., Kunsch, C., Hung, J., Li, H., Nelson, P., Olsen, H.,
 Raymond, L., Wei, Y.F., Wang, J., Xu, C., Tu, G.L., Ruben, S.M.,
 Dillon, P.J., Fannon, M.R., Rosen, C.M., Haseltine, W.A., Fields, C.,
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 6547 Suppl., 3-174 (1995)
JOURNAL

96026280
 CONTACT: Dr. PHILIP W. ARTERIALE
 CONTACT: Merilavag, AR
 Bioinformatics
 The Institute for Genomic Research
 7112 Medical Center Drive, Rockville, MD 20850 USA
 Email: arteriale@igb.org
 Fax: 3018699423
 For more availability, additional sequence and expression

PRIMER: M13-20
P-end: 3' end
DESCR: Cloning strategy is unidirectional;
Genexpress library reference is A.
automatic film reader.
Location/Qualifiers

```

1. .309
/organism="Homo sapiens"
/note="Primer M13-20"
/db_xref="taxon:9606"
/cell_type="fibroblast"
/cell_line="WI-38"
/clone_id="Stratagene cat937212 (1992)"
/clone="P11167"

```

```

BASE COUNT      88 a   56 c      54 g   111 t
ORIGIN
Query March      Score 18;  DP 38;  Length 309;
Best Local Similarity 100.0%;  Pred. No. 1.0e-02;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
DD 266 CTCACATCAGACGCTCAA 281
      |||||
07 237 CTCACATCAGACGCTCAA 254

```

20	RESULT	20	LOCUS	317 bp	EST	14-FEB-1996
DEFINITION	Y57570.3 Homo sapiens cDNA clone 276613 5'					
ACCESSION	U118064					
KEYWORDS	EST					
SOURCE	human clone-276613 primer-77 library-Soares multiple sclerosis 2NDUNG vector-p7713D (Pharmacia) with a modified polyliner					

[illegible]

ORGANISM Homo sapiens

Eukaryotes: Metazoa: Eumetazoa: Bilateria: Coelomata: Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes: Sarcopterygii: Chonata: Tetrapoda: Amniota: Mammalia: Theria: Eutheria: Archonta: Primates: Catarrhini: Homiidae: Homo.

REFERENCE AUTHORS	1 (bases 1 to 317)	TITLE
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Huttman, M., Kucaba, T., Le, M., Lennon, G., Marston, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, R., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., Wilson, R.		The Washu-Merck EST Project

Journal
Comment

Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

```

FEATURES
  source
    1. .317
      Location/Qualifiers
        /organism="Homo sapiens"
        /db_xref="GenBank:U01637"
        <!-->
      srna
    Email: celtav@vsnl.edu
    High quality sequence steps: 257
    Source: IMAGE Consortium, LNC
    Submission: LNCv1, free through LNCv1
    URL: http://www.image.llnl.gov/
    IMAGE Consortium (image@image.llnl.gov) for further information

```

```

BASE COUNT      90 a      67 c      66 g      91 t      3 others
ORIGIN
Query Match      0.9%
Best Local Similarity 100.0%:   Pred. No. 1.03e-03:
Matches 18; Conservative 0; Mismatches 0; Indels 0;
Db 292 CTCTCTCAACTCTTCTCA 309
      |||||
QY 1286 CTCTCTCAACTCTTCTCA 1303

```

RESULT	21	335 bp	mRNA	EST	21-APR
LOCUS	AA370002				
DEFINITION	Testis564 Prostate gland Homo sapiens cDNA 5' end similar to corticosteroid 11-beta-dehydrogenase, mRNA sequence				
ACCESSION	AA370002				
NID	G3022341				
KEYWORDS	EST.				
ORGANISM	Human				
ORGANISM	Homo sapiens				

REFERENCE
1. (bases 1 to 335)
Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
Eukaryotes; mitochondrial eukaryotes: Metazoa: Chordata; Holo-
vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Homo.
Homo.

Tue Nov 24 08:10:58 1998

```

/notes=Organ: endometrium; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI;
/ab_xref=ATCC (inhost:139241"
/ab_xref=ATCC (inhost:9606"
/seq="female" endometrial tumor"
/sex="female"
/seq_stage="Adult"
MENA      100 a 63 c      82 g  99 t   2 others
ORIGIN
Query Match      0.9% Score 19;  D8 4; Length 346;
Local similarity 100.0%;  Seq. Id=0.0;
Matches 19; Conservative 0; Mismatched 0; Indels 0; Gaps 0;
db 289 TTTCTGCTTCTCATGCTG 307
      |||
cp 506 TTTCTGCTTCTCATGCTG 488
      |||

RESULT 25
DESCRIPTION
ACCESSION HS_2268 PJ_504_66 277 Ancestral Human Genomic Spanning Map
VERSION 1.0 Genomic clone PJate-2268 Col-8 Roveo, genomic survey
KEYWORDS sequence.
SOURCE G85
ORGANISM Homo sapiens
PRIMATES: Catarrhini, Homnidae; Homo.
1 (bases 1 to 346)
Mahaizaa G.G., Zaktrone K.D., Smith T., Tipton S., Schmidt S.,
Craoicoff, Abplan C., Blanchard A., West A., and Hood L.,
Genomic Cloning and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Unpublished (1997)
Contact: Mahaizaa G.G. Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Fax: (206) 616-1887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Unpublished (1997)
Class MAC end: D column: 8
High quality sequence step: 346.

```

Tue Nov 24 08:10:58 1998

[illegible]

Tue Nov 24 08:10:58 1998

US-08-468-011A-1.1st

```

FEATURES             Location/Qualifiers
     source            1..346
     /organism="Homo sapiens"
     /note="Organ: sperm; Vector: pBelOAG11; BAC Clones in
     /COLI plasmid: pGEM-9608"
     /dbxref="Genebank:9608"
     /clone="Plate2368 Col-8 Row=D"
     /sequence="CtII Approved Human Genomic Sperm Library D"
     /sex="Male"
BASE COUNT          70 a 129 c 63 g 84 t
ORIGIN
      0.94; Score 19; Dlg 27; Length 346;
      100% Identical Similarity 100%; Pct. Identical=05;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      Db 29 TCATCTTCGCTCCCGCAC 47
      Cp 1657 TCAATCTTCGCTCCCGCAC 1639

RESULT 26 A0028563      349 bp     DNA          29-JUN-1998
DEFINITION      C17-HSP-2323J778 C17-HSP Homo sapiens genomic clone 2323J77,
                 genomic survey sequence...
ACCESSION      A0028563
VERSION        1
KEYWORDS       Genomic Regions
SOURCE         G548785
ORGANISM       human.
               Homo sapiens
               Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
               Primates; Hominoidea; Homodes; Homo.
REFERENCE      1 (bases 1 to 349)
AUTHORS        Adams M.D., Rounsley S.D., Field C.E., Bass S., Linher K.,
               Golden K., Barry K., Granger D., Suh E., Wille C., Shiley H.,
               Dawson M. and Venter J.C.
               Genomic Libraries and the Human Genome Project: The
               Building a Random SMC End Sequence Database for Sequence-Ready Map
               Building (1997)
               Unpublished (1997)
JOURNAL
COMMENT
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 918 0200
Fax: 301 918 0206
Email: mdamadmit@igf.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page: http://www.igf.edu/human/bac\_end\_search/bac\_end\_search.html
Seq. Project: M13 ReQuest

```

Tue Nov 24 08:10:58 1998

US-08-468-011A-1.int

```

University of Florida  
Blvd., 471 McGrew Rd., Gainesville, FL 32611-0880  
Tel.: 9043924700  
Fax: 9043929704  
Email: daniel@chir.ifs.ufl.edu.  
  
FEATURES             source  
          i . 363 /qualifiers  
            /organism='Plasmodium falciparum'  
           /clone='PFO023N'  
BASE COUNT      116 a   40 c   50 g    11 t     6 others  
ORIGIN  
Query Match       0 %; Score 19; DB 3; Length 363;  
Library Local 100%; Ped. Mod. 74e-05; Vector 363;  
Matches         1? Conserved? ? Mutations 0; Gaps 0; Caps 0;  
DB 169 GAAGCAAGAATGACATCT 187  
| | | | | | | | | | | | |  
CY 215 GAAGCAAGAATGACATCT 233  
  
RESULT 28 582324        368 bp      MWNA                EST              01-JUN-1995  
DEFINITION YH58402.s1 Homo sapiens CDNA clone 137766 3,  
ACCSSION E841751  
KEYWORDS  
SOURCE  
CDNA=clones17766 library+cosmids placenta MBVNU vector+viral  
(Pharmacia) with a modified polynucleotide non-DHIOB (ampicillin  
resistant) primer-SF6 BaitNet I Bat2-Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
AACCGAAGAATCCGGCAGCATTTTTCCTTTTTTTTTT 3'. Double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pTV7  
vector. Library went through one round of normalization. Library  
screening by Sento Soares and Nifantseva Bonaldi.  
Homo sapiens  
ORGANISM  
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Mammalia; Primates; Hominidae; Hominoidea; Homininae; Genus:  
Hominia; Archonta; Placentalis; Catarrhini; Hominiidae; Homo.  
Eutheria  
1 (bases 1 to 368)  
Miller,L., Clark,N., Duboucq,T., Buchanan,J.C.M., Lemmon,G.P., Harris,M.,  
Holman,R., Ruffalo,H., Schmitt,C.T., Calkins,D.G.  
Wilson,E.E., Matarston,R., Williamson,A., Woldmann,P. and  
Wileon.R.  
  
TITLE The Masho-Merck EST Project  
Unpublished (1995)
```


RESULT 32

Locus
LOCUS
DEFINITION
Accession
Accession
Keywords
Organism
Reference
Authors
Title
Journal
Comment

A0741392 408 bp mRNA EST
07-FEB-1998
NM6611.1; NCBI Homo sapiens cDNA clone IMAGE1286181,
mRNA sequence.
A0741392
92179584
NID
EST.
human
Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiide; Homo.
NCI (case no 408)
NCI (case no 408) ncbi.nlm.nih.gov/ncicdp
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

Contact: Robert Strauberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strauberg@nih.gov
Dr. Gerald Marti, Louis M. Bando, M.D., Ph.D., David Allman,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
Cloned by Greg Lennon, Ph.D.
Library: NCI-CDGP
Clone Sequencing Center
Distribution: NCI-CDGP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bnbp/image.html

Insert Length: 492 Std Error: 0.00
Seq primer: -40ml3 fwd. str from Amerham
High quality sequence spot: 312.
Location/Qualifiers
408
/organism="Homo sapiens"
/note=vector: pTRIP3-pac (Pharmacia) with a modified
polylinker site 1: Not I. Site 2: Eco RI. lac start strand
directional.
The following information was provided by Dr. Louis M. Bando (NCI),
provided by Dr. Louis M. Bando (NCI). Dr. David Allman
(NCI) and Dr. Gerald Marti (CBR). cDNA synthesis was
performed using the following primers:
15'-GTTACCACTCAGATGGAGCCGCCGCCTCATTTTTTTTTTTTTT-
(Pharmacia), digested with Not I and cloned into the Not I
site of the pTRIP3 vector. The resulting library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldi."

FEATURES
source

[illegible]

ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 427)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Wilson, R., Waterston, R., Williamson, A., Wohlmann, P., and The WashU-Merck EST Project
Unpublished (1995)

TITLE JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyt not found
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40M13 fwd. from Amersham
High quality sequence: 396
Location/Qualifiers
1. 427

FEATURES
source
BASE COUNT 84 a 94 c 135 g 103 t 5 others
ORIGIN
/organism="Homo sapiens"
/clone="13665"
/db_xref="taxon:9606"

Query Match 0.94; Score 19; DB 3; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 61 TGGCTGCTGCTGCTGCG 79
Cp 1474 TGGCTGCTGCTGCTGCG 1456

RESULT 36 AA017612 427 bp mRNA EST 26-NOV-1996
DEFINITION A019031 at Soares NHRP4 Homo sapiens cDNA 25-NOV-1996
similar to PIR:861209 861209 hypertension-induced protein 8-2 - rat
; mRNA sequence.
ACCESSION AA017512
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 31 TGGCTGCTGCTGCTGCG 49
Cp 1474 TGGCTGCTGCTGCTGCG 1456

RESULT 37 AA227842 427 bp mRNA EST 24-FEB-1997
DEFINITION A256d01 at Soares NHRP4 S1 Homo sapiens cDNA clone 667193 3' similar to WP:F02C12.2 CE03132 GLUCOSE 1-DEHYDROGENASE ;, mRNA sequence.
ACCESSION A256d01
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 427)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Wilson, R., Waterston, R., Williamson, A., Wohlmann, P., and The WashU-Merck EST Project
Unpublished (1995)

TITLE JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40M13 fwd. from Amersham.
High quality sequence: 396
Location/Qualifiers
1. 427

FEATURES
source
BASE COUNT 84 a 94 c 135 g 103 t 5 others
ORIGIN
/organism="Homo sapiens"
/clone="13665"
/db_xref="taxon:9606"

REFERENCE 1 (bases 1 to 427)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Wilson, R., Waterston, R., Williamson, A., Wohlmann, P., and The WashU-Merck EST Project
Unpublished (1995)

TITLE JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyt not found
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40M13 fwd. from Amersham
High quality sequence: 396
Location/Qualifiers
1. 427

FEATURES
source
BASE COUNT 92 a 94 c 137 g 103 t 1 others
ORIGIN
/organism="Homo sapiens"
/clone="13665"
/db_xref="taxon:9606"

Query Match 0.94; Score 19; DB 24; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 30 TGGCTGCTGCTGCTGCG 48
Cp 1474 TGGCTGCTGCTGCTGCG 1456

RESULT 38 AA029151 428 bp DNA GSS 30-JUN-1998
DEFINITION RPII1-3708 TV RPII1 Homo sapiens genomic clone R-3708, genomic survey sequence.
ACCESSION AA029151
KEYWORDS GSS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 428)
Adams, M.D., Broun, S.D., Field, C.E., Bass, S., Linher, K., Venter, A., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P., and The WashU-Merck EST Project
Unpublished (1997)

TITLE JOURNAL
COMMENT
Other_GSSs: RPII1-3708.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: madams@ig.org
(Pleaseredlongmed Buffalo.edu). Clones may be purchased from Research Genetics (info@resgen.com). BAC end search page.

reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260212-265223, 34088-34579, and 484488-489479.
/clone="13665"
/clone="667193"
/clone_lib="Soares NHRP4 S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/db_xref="taxon:9606"

BASE COUNT 95 a 92 c 138 g 102 t
ORIGIN
/organism="Homo sapiens"
/clone="13665"
/db_xref="taxon:9606"

Query Match 0.94; Score 19; DB 26; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.74e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 30 TGGCTGCTGCTGCTGCG 48
Cp 1474 TGGCTGCTGCTGCTGCG 1456

RESULT 38 AA029151 428 bp DNA GSS 30-JUN-1998
DEFINITION RPII1-3708 TV RPII1 Homo sapiens genomic clone R-3708, genomic survey sequence.
ACCESSION AA029151
KEYWORDS GSS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 428)
Adams, M.D., Broun, S.D., Field, C.E., Bass, S., Linher, K., Venter, A., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P., and The WashU-Merck EST Project
Unpublished (1997)

Tue Nov 24 08:10:58 1998

RESULT 44

0000000000
similar to
0000000000

```

Emmet-Buck, M.D., Ph.D.
  cDNA Library preparation: M. Bento Soares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  cDNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: MCT-CDAP clone distribution information can be
  found at: http://www.wustl.edu/genome/CDAP/
  www.bio.lni.gov/obp/image/image.html

Seq primer: -40m3 fwd. 2T from Amerham
High quality clones: 439
  location/Qualifiers
    i. 450
      /organism="Homo sapiens"
      /vector="pGEM-1" (Pharmacia) with a modified
      polylinker 1st strand cDNA template. Cloned
      germ cell tumors, and was then primed with a Not I -
      oligo(dT) primer. Double stranded cDNA was ligated to Eco
      RI adaptors (Pharmacia) digested with Not I, and cloned
      into the MCT-CDAP library. The MCT-CDAP library
      vector. Library is normalized. Library was constructed by
      Bento Soares and M. Fatima Bonaldo.
      /DB_xref="taxon:9606"
      /clone="Homo sapiens"
      /clone_id="MCT-CDAP"
      /clone_name="MCT-CDAP"
      /tissue_type="pooled germ cell tumors"
      /lab_host="DB10"
      142 a 95 c 63 g 150 t
      0.94; Score 18; DB 17; Length 450;
      Beat Local Similarity 100.0; Pred.No. 1.03e-03;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 145 CTGTCAGCTCTCTTCA 162
QY 1377 CTGTCAGCTCTCTTCA 1294

RESULT 47
LOCUS AA393693 451 bp mRNA EST
DEFINITION Homo sapiens total testis WDRN98, ov. Homo sapiens cDNA clone
755442, 1.5 kb; similar to NF105747, CEB7544, DENDROGENASE 1, mRNA
sequence.
ACCESSION AA393693
KEYWORDS NID
KEYWORDS NID
KEYWORDS NID
KEYWORDS NID
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Primates; Eutheria; Mammalia; Eutheria; Primates; Carnivora; Homidae;

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[illegible]

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